

Submitted (APR-2002) to the EMBL/GenBank/DBJ databases.

RL EMBL; AF499613; AAM19249.1; -.
DR MGD; MGI:2179523; Fcrl3.
DR GO; GO:0004872; F:receptor activity; IEA.
DR InterPro; IPR003599; Ig.
DR InterPro; IPR007110; Ig-like.
DR Pfam; PF00047; Ig; 2.
DR SMART; SM00409; IG; 2.
DR PROSITE; PS00835; IG_LIKE; 2.
KW Receptor.
SQ SEQUENCE 249 AA; 28382 MW; 3DEAF3D935BEF5CD CRC64;

Query Match 34.2%; Score 367; DB 11; Length 249;
Best Local Similarity 41.1%; Pred. No. 1.2e-25;
Matches 76; Conservative 33; Mismatches 76; Indels 0; Gaps 0;

QY 10 LLCVALLFFAPDGVLAVPQPKVSLNPPWNRIFKGNVTLTCGNFFVSSSTKWFHNGS 69
DB 5 LLPTALVLTAFSGIOAGLQKAVNLDPKVRLVEEDSVTLRCQGTFFSPDINSIKWFHNS 64
QY 70 LSEETNSLINVAKFSDSGEYKCOHQVNESEPVYLEVFSDFMLLLQASAEVVMGQPLF 129
DB 65 LIPHQDANYVIQASARVKGSGMYRCQTALSTISDPVQLEHVGWLLQLTTKWLFOEGDPIH 124
QY 130 LRCHGWRNDVYKVIYKDGKALKYWNHNISITNATVEDSGTYCTGKWKQJDIYSEPL 189
DB 125 LRCHSWQNRPVKVTYILQNGKGYKHENSELPKPKATHNDGSGYFCRGLIGHNKKSSAS 184
QY 190 LNIIV 194
DB 185 FRISL 189

RESULT 12
QYQJ5 PRELIMINARY; PRT; 372 AA.

AC Q7YQJ5; (Created)
DT 01-OCT-2003 (TRENBLrel. 25, Last sequence update)
DT 01-OCT-2003 (TRENBLrel. 25, Last annotation update)
DE High affinity IGG Fc gamma receptor 1.
GN FCGAMMARI.
OS Canis familiaris (Dog).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Euthera; Carnivora; Fissipedia; Canidae; Canis.
OX NCBI_TaxID=9615;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=Shiba; TISSUE=Cutaneous;
RX MEDLINE=22777889; PubMed=12811428;
RA Nakamura R., Sato Y., Takagi K., Sasaki N., Sawada J., Kitani S.,
RA Teshima R.;
RT "Presence and primary sequence of a high-affinity IGG receptor on
RT canine mastocytoma (CM-MC) cells."
RL Immunogenetics 55:271-274 (2003).
DR EMBL; AB101519; BAC80263.1; -.
KW Receptor.
SQ SEQUENCE 372 AA; 42336 MW; BC04026CD198049D CRC64;

Query Match 34.2%; Score 366.5; DB 6; Length 372;
Best Local Similarity 39.1%; Pred. No. 2.2e-25;
Matches 72; Conservative 34; Mismatches 77; Indels 1; Gaps 1;

QY 11 LLCVALLFFAPDGVLAVPQPKVSLNPPWNRIFKGNVTLTCGNFFVSSSTKWFHNGSL 70
DB 3 LLTVLLWVPAQAQTDVKAIVTLQPPWVSPQESVTLWCCEGPHLPQGSSTQWFLNGTA 62
QY 71 SEETNSLINVAKFSDSGEYKCOHQVNESEPVYLEVFSDFMLLLQASAEVVMGQPLF 130
DB 63 TOTLTTPRYIAAASVNDNGEYRCQTLGSLVLSPIQGIHRDWLILQVSRVTEGEPLTL 122
QY 131 LRCHGWRNDVYKVIYKDGKALKYWNHNISITNATVEDSGTYCTGKWKQJDIYSEPL 190

RESULT 10
Q8SPW2 PRELIMINARY; PRT; 254 AA.

AC Q8SPW2;
DT 01-JUN-2002 (TRENBLrel. 21, Created)
DT 01-JUN-2002 (TRENBLrel. 21, Last sequence update)
DT 01-OCT-2003 (TRENBLrel. 25, Last annotation update)
DE Fc gamma receptor IIa.
OS Macaca fascicularis (Crab eating macaque) (Cynomolgus monkey).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Euthera; Primates; Catarrhini; Cercopithecoidea;
OC Cercopithecoidea; Macaca.
OX NCBI_TaxID=9541;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Spleen;
RA Namenuk A.K., Hong K., Meng Y.G., Shields R.L., Cronwell M.E.M.,
RA Presta L.G.;
RT "Binding of human IGG to cynomolgus FcR."
RL Submitted (FEB-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF485815; AAL92098.1; -.
DR GO; GO:0004872; F:receptor activity; IEA.
DR InterPro; IPR003599; Ig.
DR InterPro; IPR007110; Ig-like.
DR Pfam; PF00047; Ig; 2.
DR SMART; SM00409; IG; 2.
DR PROSITE; PS00835; IG_LIKE; 2.
KW Receptor.
SQ SEQUENCE 254 AA; 29120 MW; 11A48E6B3A34AF7B CRC64;

Query Match 34.4%; Score 369.5; DB 6; Length 254;
Best Local Similarity 42.2%; Pred. No. 7.2e-26;
Matches 79; Conservative 31; Mismatches 74; Indels 3; Gaps 2;

QY 10 LLCVALLFFAPDGVLA--VPQPKVSLNPPWNRIFKGNVTLTCGNFFVSSSTKWFH 67
DB 5 LLPTALLVLSAGRAEDLP-KAVFLEPQWVLEKRDVTLKCOGAYSPEDNSTKWFH 63
QY 68 GSISETNSLINVAKFSDSGEYKCOHQVNESEPVYLEVFSDFMLLLQASAEVVMGQPL 127
DB 64 ESLISSQTSYFFAAARVNSGEVRCQTSLSLSDPQLEVHIGWLLQAPRVVKEES 123
QY 128 LFRCHGWRNDVYKVIYKDGKALKYWNHNISITNATVEDSGTYCTGKWKQJDIYSEPL 187
DB 124 IHLRCHSWQNTLLHKVYTLQNGKGRKYFHQNSDFYIPKATLKDSDGSGYFCRGLIGSKNVSS 183
QY 188 EPLNITV 194
DB 184 ETVNITI 190

RESULT 11
Q8R477 PRELIMINARY; PRT; 249 AA.

AC Q8R477;
DT 01-JUN-2002 (TRENBLrel. 21, Created)
DT 01-JUN-2002 (TRENBLrel. 21, Last sequence update)
DT 01-OCT-2003 (TRENBLrel. 25, Last annotation update)
DE Transmembrane receptor CD16-2.
GN Fcrl3.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Euthera; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL; TISSUE=Liver;
RA Mechetina L.V., Najakshin A.M., Alabyev B.Y., Chikaev N.A.,
RA Tarantin A.V.;
RT "Identification of CD16-2, a novel mouse receptor homologous to
RT CD16/FcgrIII.";

```

Db 123 RCHGWNKLVYVNFYQNGTVLKFSPQNSEFTILKTLHNGIYHCSA-MGKHRYESAGV 181
QY 191 NITV 194
Db 182 SITI 185

RESULT 13
Q8R2R4 PRELIMINARY; PRT; 249 AA.
ID Q8R2R4 AC Q8R2R4;
DT 01-JUN-2002 (TrEMBLrel. 21, Created)
DT 01-JUN-2002 (TrEMBLrel. 21, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Hypothetical protein.
GN FCRL3.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]_TaxID=10090;
RP SEQUENCE FROM N.A.
RA Strausberg R.;
RL Submitted (APR-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL; BC027310; AAH27310.1; -.
DR MGD; MGI:2179523; Fcrl3.
DR InterPro; IPR003599; Ig.
DR InterPro; IPR007110; Ig-like.
DR Pfam; PF00047; Ig; 2.
DR SMART; SM00409; IG; 2.
DR PROSITE; PS0835; IG LIKE; 2.
KW Hypothetical protein.
SQ SEQUENCE 249 AA; 28372 MW; 740D6BE8E1536224 CRC64;

Query Match 34.0%; Score 365; DB 11; Length 249;
Best Local Similarity 41.1%; Pred. No. 1.8e-25;
Matches 76; Conservative 33; Mismatches 76; Indels 0; Gaps 0;

QY 10 LLCVALLFFAPDGLAVPQPKVSLNPPWNRIFKGENVTLTCNGNNFEVSTKWFHGS 69
Db 5 LLPTALVLTASGIQAGLQKAVNLDPKVRVLEDSVTLRCQGTFFSPDENSINWFHNS 64
QY 70 LSEETNSLNINNAKPEDSGYKCOHQVNESEPVYLEVFSMDLLQLQASAEVVMGQPLF 129
Db 65 LIPQDANYVTQSAKVDKSGMYRCQTALSTISDPVQLVHMGWLLLTQTKWLFQEGDPIH 124
QY 130 LRCHGWRNDVYKVIYKDGKALKYENHNISITNATVEDSGTYCTGKVWQLDYESEP 189
Db 125 LRCHSWQNPVRKVTYSQNGKGYFHNSELLIPKATHNDSSGYPFCRGLIGNKSSAS 184
QY 190 LNITV 194
Db 185 FRISL 189

RESULT 14
Q9N2I6 PRELIMINARY; PRT; 249 AA.
ID Q9N2I6 AC Q9N2I6;
DT 01-OCT-2000 (TrEMBLrel. 15, Created)
DT 01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE CD16.
GN CD16.
OS Felis silvestris catus (Cat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Carnivora; Fissipedia; Felidae; Felis.
OX NCBI_TaxID=9685;
RN [1]_TaxID=9685;
RP SEQUENCE FROM N.A.
RA Nishimura Y., Miyazawa T., Ikeda Y., Izumiya Y., Nakamura K., Sato E.,
RA Mikami T., Takahashi E.;

```

```

RT "Molecular cloning and sequencing of the cDNA encoding the feline
RT Fc(gamma)RIIIA (CD16) homologue.";
RL Vet. Immunol. Immunopathol. 73:353-359(2000).
DR EMBL; AB025314; BAA92347.1; -.
DR InterPro; IPR003599; Ig.
DR InterPro; IPR007110; Ig-like.
DR Pfam; PF00047; Ig; 2.
DR SMART; SM00409; IG; 2.
DR PROSITE; PS0835; IG LIKE; 2.
SQ SEQUENCE 249 AA; 27902 MW; 683528C68A7CA37A CRC64;

Query Match 33.8%; Score 363; DB 6; Length 249;
Best Local Similarity 42.0%; Pred. No. 2.8e-25;
Matches 79; Conservative 25; Mismatches 80; Indels 4; Gaps 1;

QY 7 SPTLLCVALLFFAPDGLAVPQPKVSLNPPWNRIFKGENVTLTCNGNNFEVSTKWFH 66
Db 6 SPT---ALLLVASAGTRADLSKAMVLEPEWNRVLSVDSGVILKCEGAYPPCDNSAQW 61
QY 67 NGSLSSETNSLNINNAKPEDSGYKCOHQVNESEPVYLEVFSMDLLQLQASAEVVMGQ 126
Db 62 NGSVIPHRAPSYSEIARSEDSEYKCOGTGLSEADPVQLVHTGWLQLQAPRWVFGED 121
QY 127 PLFLRCHGWRNDVYKVIYKDGKALKYENHNISITNATVEDSGTYCTGKVWQLDYE 186
Db 122 TIQLRCHSWKNTVQKQVQFDGCRGMFFHKNSDYIPKATSKHSGSYFCRGLIGNK 181
QY 187 SEPLNITV 194
Db 182 SEAVNITV 189

RESULT 15
Q9ES92 PRELIMINARY; PRT; 261 AA.
ID Q9ES92 AC Q9ES92;
DT 01-WAR-2001 (TrEMBLrel. 16, Created)
DT 01-WAR-2001 (TrEMBLrel. 16, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Fc gamma receptor II.
GN FCGR3.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]_TaxID=10090;
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6;
RA Fossati Jimack L., Boucrot E., Izui S.;
RT "Mouse Fc gamma RII: identification and characterization of a new
RT allele in C57BL/6 mice.";
RL Submitted (OCT-1999) to the EMBL/GenBank/DBJ databases.
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6J; TISSUE=Ovary, and Uterus;
RX MEDLINE=22354683; PubMed=12466851;
RA The FANTOM Consortium,
RA The RIKEN Genome Exploration Research Group Phase I & II Team;
RT "Analysis of the mouse transcriptome based on functional annotation of
RT 60,770 full-length cDNAs.";
RL Nature 420:563-573(2002).
DR EMBL; AF197930; AAG28520.1; -.
DR EMBL; AK077227; BAC36696.1; -.
DR MGD; MGI:95500; Fcgr3.
DR GO; GO:0004872; F:receptor activity; IEA.
DR InterPro; IPR003599; Ig.
DR InterPro; IPR007110; Ig-like.
DR Pfam; PF00047; Ig; 2.
DR SMART; SM00409; IG; 2.
DR PROSITE; PS0835; IG LIKE; 2.
KW Receptor.
SQ SEQUENCE 261 AA; 30098 MW; 9C8570E032F94730 CRC64;

```

Query Match 33.8%; Score 363; DB 11; Length 261;
Best Local Similarity 40.5%; Pred. No. 2.9e-25;
Matches 75; Conservative 31; Mismatches 77; Indels 2; Gaps 2;

QY 11 LCVALLFFAPDGYLAVPQPKVSLNPPMNRIFKGENVILTCNGNNPFFVSVSTKWPHN-GS 69
| : | | | | | : | | | : | : | | | : | | | | |
Db 16 LTILLFAFADRQSAALPKAVVKLDPPMTIQVLKEDMTLMCEGTHNPGNSSTQWFHWS 75
| : | | | | | : | | | : | : | | | : | | | | |
QY 70 LSEETNSSLNIVNAKEFDSGEYKCOHQVNESEPPVYLFVSDWLLIQAASAEVVMGQPLF 129
| : | | | | | : | | | : | : | | | | | | | | |
Db 76 IRSQVQSYTF-KATVNDSEYRCQEQRLSDPVDLGVISDWLLQLTPQRFLEGETIT 134
| : | | | | | : | | | : | : | | | | | | | | |
QY 130 LRCHGWRNWDVKVIYKDGKALKYWYENHNISITNATVEDSGTYCTGKVMQLDYSEPP 189
| | | | | : : : : : : : : : : : | | | | : : : : :
Db 135 LRCHSWRNKLLARISFFHNEKSVRYHHYKSNFSIPKANHSHSGDYVCKGSLGSTQHQSKP 194
| : | | | | | : | | | : | : | | | | | | | | |
QY 190 LNITY 194
| : | | | | | : | | | : | : | | | | | | | | |
Db 195 VTITV 199
| : | | | | | : | | | : | : | | | | | | | | |

Search completed: October 6, 2004, 09:07:03
Job time : 31.9965 secs

This Page Blank (uspio)

GenCore version 5.1.6
Copyright (c) 1993 - 2004 CompuGen Ltd.

OM nucleic - nucleic search, using sw model
Run on: October 10, 2004, 11:14:29 ; Search time 2246.88 Seconds
(without alignments)
9953.801 Million cell updates/sec
Title: US-10-763-400-12
Perfect score: 516
Sequence: 1 gtcctcagaacctaaggt.....acattactgtaataaaagct 516
Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0
Searched: 3470272 seqs, 21671516995 residues
Total number of hits satisfying chosen parameters: 6940544
Minimum DB seq length: 0
Maximum DB seq length: 2000000000
Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :

- GenEmbl.*
1: gb.ba.*
2: gb.htg.*
3: gb.in.*
4: gb.om.*
5: gb.ov.*
6: gb.pat.*
7: gb.ph.*
8: gb.pl.*
9: gb.pr.*
10: gb.ro.*
11: gb.sts.*
12: gb.sy.*
13: gb.un.*
14: gb.vi.*
15: em.ba.*
16: em.fun.*
17: em.hum.*
18: em.in.*
19: em.mu.*
20: em.om.*
21: em.or.*
22: em.ov.*
23: em.pat.*
24: em.ph.*
25: em.pl.*
26: em.ro.*
27: em.sts.*
28: em.un.*
29: em.vi.*
30: em.htg.hum.*
31: em.htg.inv.*
32: em.htg.other.*
33: em.htg.mus.*
34: em.htg.pln.*
35: em.htg.rod.*
36: em.htg.mam.*
37: em.htg.vrt.*
38: em.sy.*
39: em.htgo.hum.*
40: em.htgo.mus.*
41: em.htgo.other.*

Pred. No. is the number of results predicted by chance to have a

score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	516	100.0	516	6	AR175487
2	516	100.0	516	6	AX074296 Sequence
3	516	100.0	516	6	AX074298 Sequence
4	516	100.0	528	6	AX274969 Sequence
5	516	100.0	560	6	BD264322 Recombina
6	516	100.0	560	6	AX026805 Sequence
7	516	100.0	591	6	AR175486 Sequence
8	516	100.0	591	6	AX074293 Sequence
9	516	100.0	591	6	AX074295 Sequence
10	516	100.0	696	6	AX074290 Sequence
11	516	100.0	696	6	AX074292 Sequence
12	516	100.0	699	6	AR175483 Sequence
13	516	100.0	713	6	E07699 CDNA encodi
14	516	100.0	773	6	AR219964 Sequence
15	516	100.0	774	6	AR175481 Sequence
16	516	100.0	774	6	AR175482 Sequence
17	516	100.0	1068	6	A21606 human FC ep
18	516	100.0	1068	6	BD264325 Recombina
19	516	100.0	1068	6	AX026808 Sequence
20	516	100.0	1081	9	HUMMC1AA
21	516	100.0	1102	9	BC005912 Homo sapi
22	516	100.0	1106	9	BC015195 Homo sapi
23	516	100.0	1174	6	AR123794 Sequence
24	516	100.0	1198	6	AR175479 Sequence
25	516	100.0	1198	6	AR175480 Sequence
26	516	100.0	1198	6	AX074287 Sequence
27	516	100.0	1198	6	AX074289 Sequence
28	516	100.0	1198	6	AX101304 Sequence
29	516	100.0	1198	6	AX335621 Sequence
30	516	100.0	1198	9	HSFCERI
31	516	100.0	1908	6	AX074315 Sequence
32	516	100.0	1908	6	AX074317 Sequence
33	516	100.0	1983	6	AX074312 Sequence
34	516	100.0	1983	6	AX074314 Sequence
35	516	100.0	2193	6	AX074306 Sequence
36	516	100.0	2193	6	AX074308 Sequence
37	516	100.0	2268	6	AX074303 Sequence
38	516	100.0	2268	6	AX074305 Sequence
39	516	100.0	2955	6	AR219962 Sequence
40	511.2	99.1	1198	6	I09686
41	508.4	98.4	516	6	BD267592
42	504.4	97.8	528	6	BD267591
43	503.2	97.5	528	6	AX274571
44	293.8	56.9	1082	4	OAR18205
45	287.2	55.7	603	6	AR344296 Sequence

ALIGNMENTS

RESULT 1
AR175487
LOCUS
DEFINITION
ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM
REFERENCE
AUTHORS
TITLE
JOURNAL
FEATURES

AR175487
Sequence 12 from patent US 6309832.
AR175487
AR175487.1 GI:17916786
Unknown.
Unknown.
Unclassified.
1 (bases 1 to 516)
Frank.G.R., Porter,J.P., Rushlow,K.E. and Wassom,D.L.
Method to detect IGE
Patent: US 6309832-A 12 30-OCT-2001;
Location/Qualifiers

516 bp
DNA
linear
PAT 17-DEC-2001

```
source 1..516
/organism="unknown"
/mol_type="unassigned DNA"

ORIGIN
Query Match 100.0%; Score 516; DB 6; Length 516;
Best Local Similarity 100.0%; Pred. No. 2.2e-147;
Matches 516; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GTCCCTCAGAACCTTAAGTCTCCTTGAACCCCTCCATGGAATAGAAATATTAAAGGAGAG 60
DB 1 GTCCCTCAGAACCTTAAGTCTCCTTGAACCCCTCCATGGAATAGAAATATTAAAGGAGAG 60
QY 61 AATGTGACTCTTACATGTAATGGAACAAATTTCTTGAAGTCAGTTCACCAATGGTTC 120
DB 61 AATGTGACTCTTACATGTAATGGAACAAATTTCTTGAAGTCAGTTCACCAATGGTTC 120
QY 121 CACAATGGCAGCCTTTCAAGAGAGACAAATTCAGATTGGAATATTGTAATGCCAAATTT 180
DB 121 CACAATGGCAGCCTTTCAAGAGAGACAAATTCAGATTGGAATATTGTAATGCCAAATTT 180
QY 181 GAAGACAGTGAGATACAAATGTCAGCACCAACCAAGTTAATGAGAGTGAACCTGTGTAC 240
DB 181 GAAGACAGTGAGATACAAATGTCAGCACCAACCAAGTTAATGAGAGTGAACCTGTGTAC 240
QY 241 CTGGAAGTCTTCAAGTACTGGCTGCTCCTTCAGGCTCTGCTGAGGTGGTGATGGAGGC 300
DB 241 CTGGAAGTCTTCAAGTACTGGCTGCTCCTTCAGGCTCTGCTGAGGTGGTGATGGAGGC 300
QY 301 CAGCCCTCTTCTCAGTGCCATGCTGCTGAGGAACTGGAGTGTGTACAAGGTGATCTAT 360
DB 301 CAGCCCTCTTCTCAGTGCCATGCTGCTGAGGAACTGGAGTGTGTACAAGGTGATCTAT 360
QY 361 TATAAGGATGTGAAGCTCTCAAGTACTGGTATGAGAACCAACATCTCCATTACAAAT 420
DB 361 TATAAGGATGTGAAGCTCTCAAGTACTGGTATGAGAACCAACATCTCCATTACAAAT 420
QY 421 GCCACAGTTGAAGACAGTGGAACTTACTGTACGGGCAAGTGTGGCAGCTGGACTAT 480
DB 421 GCCACAGTTGAAGACAGTGGAACTTACTGTACGGGCAAGTGTGGCAGCTGGACTAT 480
QY 481 GAGTCTGAGCCCTCAACATTACTGTATAAAGCT 516
DB 481 GAGTCTGAGCCCTCAACATTACTGTATAAAGCT 516

RESULT 2
AX074296 516 bp DNA linear PAT 06-FEB-2001
LOCUS
DEFINITION Sequence 10 from Patent WO0104310.
ACCESSION AX074296
VERSION AX074296.1 GI:12710483
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE
1 Weber E.R., Wood, K.V. and Hall, M.P.
Fc epsilon receptor-luminescence inducing protein chimeric nucleic
acid molecules, fusion proteins and uses thereof
Patent: WO 0104310-A 10 18-JAN-2001;
JOURNAL Heiska Corporation (US); PROMEGA CORPORATION (US)
FEATURES
source
1..516
/organism="Homo sapiens"
/mol_type="unassigned DNA"
<1..>516
/notes="unnamed protein product"
/codon_start=1
/protein_id="CAC28466.1"
/db_xref="GI:12710484"

CDS
Query Match 100.0%; Score 516; DB 6; Length 516;
Best Local Similarity 100.0%; Pred. No. 2.2e-147;
Matches 516; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GTCCCTCAGAACCTTAAGTCTCCTTGAACCCCTCCATGGAATAGAAATATTAAAGGAGAG 60
DB 1 GTCCCTCAGAACCTTAAGTCTCCTTGAACCCCTCCATGGAATAGAAATATTAAAGGAGAG 60
QY 61 AATGTGACTCTTACATGTAATGGAACAAATTTCTTGAAGTCAGTTCACCAATGGTTC 120
DB 61 AATGTGACTCTTACATGTAATGGAACAAATTTCTTGAAGTCAGTTCACCAATGGTTC 120
QY 121 CACAATGGCAGCCTTTCAAGAGAGACAAATTCAGATTGGAATATTGTAATGCCAAATTT 180
DB 121 CACAATGGCAGCCTTTCAAGAGAGACAAATTCAGATTGGAATATTGTAATGCCAAATTT 180
QY 181 GAAGACAGTGAGATACAAATGTCAGCACCAACCAAGTTAATGAGAGTGAACCTGTGTAC 240
DB 181 GAAGACAGTGAGATACAAATGTCAGCACCAACCAAGTTAATGAGAGTGAACCTGTGTAC 240
QY 241 CTGGAAGTCTTCAAGTACTGGCTGCTCCTTCAGGCTCTGCTGAGGTGGTGATGGAGGC 300
DB 241 CTGGAAGTCTTCAAGTACTGGCTGCTCCTTCAGGCTCTGCTGAGGTGGTGATGGAGGC 300
QY 301 CAGCCCTCTTCTCAGTGCCATGCTGCTGAGGAACTGGAGTGTGTACAAGGTGATCTAT 360
DB 301 CAGCCCTCTTCTCAGTGCCATGCTGCTGAGGAACTGGAGTGTGTACAAGGTGATCTAT 360
QY 361 TATAAGGATGTGAAGCTCTCAAGTACTGGTATGAGAACCAACATCTCCATTACAAAT 420
DB 361 TATAAGGATGTGAAGCTCTCAAGTACTGGTATGAGAACCAACATCTCCATTACAAAT 420
QY 421 GCCACAGTTGAAGACAGTGGAACTTACTGTACGGGCAAGTGTGGCAGCTGGACTAT 480
DB 421 GCCACAGTTGAAGACAGTGGAACTTACTGTACGGGCAAGTGTGGCAGCTGGACTAT 480
QY 481 GAGTCTGAGCCCTCAACATTACTGTATAAAGCT 516
DB 481 GAGTCTGAGCCCTCAACATTACTGTATAAAGCT 516

RESULT 3
AX074296 516 bp DNA linear PAT 06-FEB-2001
LOCUS
DEFINITION Sequence 12 from Patent WO0104310.
ACCESSION AX074296
VERSION AX074296.1 GI:12710485
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE
1 Weber E.R., Wood, K.V. and Hall, M.P.
Fc epsilon receptor-luminescence inducing protein chimeric nucleic
acid molecules, fusion proteins and uses thereof
Patent: WO 0104310-A 12 18-JAN-2001;
JOURNAL Heiska Corporation (US); PROMEGA CORPORATION (US)
FEATURES
source
1..516
/organism="Homo sapiens"
/mol_type="unassigned DNA"
/db_xref="taxon:9606"
<1..>516
/notes="unnamed protein product"
/codon_start=1
/protein_id="CAC28466.1"
/db_xref="GI:12710484"

ORIGIN
Query Match 100.0%; Score 516; DB 6; Length 516;
Best Local Similarity 100.0%; Pred. No. 2.2e-147;
Matches 516; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GTCCCTCAGAACCTTAAGTCTCCTTGAACCCCTCCATGGAATAGAAATATTAAAGGAGAG 60
DB 1 GTCCCTCAGAACCTTAAGTCTCCTTGAACCCCTCCATGGAATAGAAATATTAAAGGAGAG 60
QY 61 AATGTGACTCTTACATGTAATGGAACAAATTTCTTGAAGTCAGTTCACCAATGGTTC 120
DB 61 AATGTGACTCTTACATGTAATGGAACAAATTTCTTGAAGTCAGTTCACCAATGGTTC 120
QY 121 CACAATGGCAGCCTTTCAAGAGAGACAAATTCAGATTGGAATATTGTAATGCCAAATTT 180
DB 121 CACAATGGCAGCCTTTCAAGAGAGACAAATTCAGATTGGAATATTGTAATGCCAAATTT 180
QY 181 GAAGACAGTGAGATACAAATGTCAGCACCAACCAAGTTAATGAGAGTGAACCTGTGTAC 240
DB 181 GAAGACAGTGAGATACAAATGTCAGCACCAACCAAGTTAATGAGAGTGAACCTGTGTAC 240
QY 241 CTGGAAGTCTTCAAGTACTGGCTGCTCCTTCAGGCTCTGCTGAGGTGGTGATGGAGGC 300
DB 241 CTGGAAGTCTTCAAGTACTGGCTGCTCCTTCAGGCTCTGCTGAGGTGGTGATGGAGGC 300
QY 301 CAGCCCTCTTCTCAGTGCCATGCTGCTGAGGAACTGGAGTGTGTACAAGGTGATCTAT 360
DB 301 CAGCCCTCTTCTCAGTGCCATGCTGCTGAGGAACTGGAGTGTGTACAAGGTGATCTAT 360
QY 361 TATAAGGATGTGAAGCTCTCAAGTACTGGTATGAGAACCAACATCTCCATTACAAAT 420
DB 361 TATAAGGATGTGAAGCTCTCAAGTACTGGTATGAGAACCAACATCTCCATTACAAAT 420
QY 421 GCCACAGTTGAAGACAGTGGAACTTACTGTACGGGCAAGTGTGGCAGCTGGACTAT 480
DB 421 GCCACAGTTGAAGACAGTGGAACTTACTGTACGGGCAAGTGTGGCAGCTGGACTAT 480
QY 481 GAGTCTGAGCCCTCAACATTACTGTATAAAGCT 516
DB 481 GAGTCTGAGCCCTCAACATTACTGTATAAAGCT 516

/db_xref="REMTREMBL:CAC28466"
/translation="VPQPKVSLNPPNRRIFKGENVTUICNGNPFVSVSTKWFHNGS
LSEETSNLSINIVNAKFEDESKYKQHOVNESEPVYLEVFDWLLQLQASAVWMEQGP
LFLRGHWNRNDVYKVIYKDDGEALKWYENHNISITNATVEDSGTYYCTGKMWQLDY
ESEPLNITVIKA"
```

Best Local Similarity 100.0%; Pred. No. 2.2e-147; Matches 516; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GTCCCTCAGAACTTAAGTCTCTTGAACCCCTCCATGGAATAGAAATATTAAAGGAGAG 60

Db 516 GTCCCTCAGAACTTAAGTCTCTTGAACCCCTCCATGGAATAGAAATATTAAAGGAGAG 457

QY 61 AATGTGACTTTACATGTAATGGGAACAATTTCTTTGAAGTCAGTTCACCAAAATGGTTC 120

Db 456 AATGTGACTTTACATGTAATGGGAACAATTTCTTTGAAGTCAGTTCACCAAAATGGTTC 397

QY 121 CACAATGGAGCCCTTTCAGAGAGACAATTTCAAGTTTGAATTTGTAATGGCCAAATTT 180

Db 396 CACAATGGAGCCCTTTCAGAGAGACAATTTCAAGTTTGAATTTGTAATGGCCAAATTT 337

QY 181 GAAGACAGTGGAGAAATACAAATTTTCAGCACCACCAAGTTAATGAGAGTGAACCTGTGTAC 240

Db 336 GAAGACAGTGGAGAAATACAAATTTTCAGCACCACCAAGTTAATGAGAGTGAACCTGTGTAC 277

QY 241 CTGGAAGTCTTCAGTGAAGTCTCTTCAAGGCTCTCTGAGGCTGATGGAGGCG 300

Db 276 CTGGAAGTCTTCAGTGAAGTCTCTTCAAGGCTCTCTGAGGCTGATGGAGGCG 217

QY 301 CAGCCCTCTTCTCAGTGGCCATGTTGGAGGAACTGGATGTGTACAAAGTGTATCTAT 360

Db 216 CAGCCCTCTTCTCAGTGGCCATGTTGGAGGAACTGGATGTGTACAAAGTGTATCTAT 157

QY 361 TATAAGATGGTGAAGCTCTCAAGTCTGATGAGACCAACCAATCTCCATTACAAAT 420

Db 156 TATAAGATGGTGAAGCTCTCAAGTCTGATGAGACCAACCAATCTCCATTACAAAT 97

QY 421 GCCACAGTTGAGACAGTGGACCTTACTCTGACGGCAAGTGTGGCAGCTGGACTAT 480

Db 96 GCCACAGTTGAGACAGTGGACCTTACTCTGACGGCAAGTGTGGCAGCTGGACTAT 37

QY 481 GAGTCTGAGCCCTCAACATTACTGTAAATAAAGCT 516

Db 36 GAGTCTGAGCCCTCAACATTACTGTAAATAAAGCT 1

RESULT 4

AX274969

LOCUS

Sequence 1 from Patent WO0169253.

AX274969

AX274969.1 GI:16547592

Keywords

Homo sapiens (human)

ORGANISM

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

REFERENCE

Jardetzky, T.S., Garman, S.C., Wurzburg, B.A. and Kinet, J.P.

Three-dimensional model of a complex between a fc epsilon receptor alpha chain and a fc region of an ige antibody and uses thereof

Patent: WO 0169253-A 1 20-SEP-2001;

Heeska Corporation (US); Northwestern University (US)

FEATURES

source

1..528

/organism="Homo sapiens"

/mol_type="unassigned DNA"

/db_xref="taxon:9606"

<1..>528

/note="unnamed protein product"

/codon_start=1

/protein_id="CAD10319.1"

/db_xref="GI:16547593"

/translation="VPOKPKVSLNPNRIFKGNVTLTCNGNNPFVSVSTKWFHNGS LSFTNSLLINVAKEFDSEYKCOHQVNESEPVYLEVFDLLOAARVMEQGP LFLRCHGRNWDVVKVYYKDGALKWYENHNISITNATVEDSGTYCTGKVMQLDY ESEPLNITVIKAPREK"

CDS

ORIGIN

Query Match 100.0%; Score 516; DB 6; Length 528; Best Local Similarity 100.0%; Pred. No. 2.2e-147; Matches 516; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GTCCCTCAGAACTTAAGTCTCTTGAACCCCTCCATGGAATAGAAATATTAAAGGAGAG 60

Db 1 GTCCCTCAGAACTTAAGTCTCTTGAACCCCTCCATGGAATAGAAATATTAAAGGAGAG 60

QY 61 AATGTGACTTTACATGTAATGGGAACAATTTCTTTGAAGTCAGTTCACCAAAATGGTTC 120

Db 61 AATGTGACTTTACATGTAATGGGAACAATTTCTTTGAAGTCAGTTCACCAAAATGGTTC 120

QY 121 CACAATGGAGCCCTTTCAGAGAGACAATTTCAAGTTTGAATTTGTAATGGCCAAATTT 180

Db 121 CACAATGGAGCCCTTTCAGAGAGACAATTTCAAGTTTGAATTTGTAATGGCCAAATTT 180

QY 181 GAAGACAGTGGAGAAATACAAATTTTCAGCACCACCAAGTTAATGAGAGTGAACCTGTGTAC 240

Db 181 GAAGACAGTGGAGAAATACAAATTTTCAGCACCACCAAGTTAATGAGAGTGAACCTGTGTAC 240

QY 241 CTGGAAGTCTTCAGTGAAGTCTCTTCAAGGCTCTCTGAGGCTGATGGAGGCG 300

Db 241 CTGGAAGTCTTCAGTGAAGTCTCTTCAAGGCTCTCTGAGGCTGATGGAGGCG 300

QY 301 CAGCCCTCTTCTCAGTGGCCATGTTGGAGGAACTGGATGTGTACAAAGTGTATCTAT 360

Db 301 CAGCCCTCTTCTCAGTGGCCATGTTGGAGGAACTGGATGTGTACAAAGTGTATCTAT 360

QY 361 TATAAGATGGTGAAGCTCTCAAGTCTGATGAGACCAACCAATCTCCATTACAAAT 420

Db 361 TATAAGATGGTGAAGCTCTCAAGTCTGATGAGACCAACCAATCTCCATTACAAAT 420

QY 421 GCCACAGTTGAGACAGTGGACCTTACTCTGACGGCAAGTGTGGCAGCTGGACTAT 480

Db 421 GCCACAGTTGAGACAGTGGACCTTACTCTGACGGCAAGTGTGGCAGCTGGACTAT 480

QY 481 GAGTCTGAGCCCTCAACATTACTGTAAATAAAGCT 516

Db 481 GAGTCTGAGCCCTCAACATTACTGTAAATAAAGCT 516

RESULT 5

BD264322

LOCUS

Recombinant soluble Fc receptors.

BD264322

BD264322.1 GI:33074090

VERSION

JP 2002531086-A/5.

KEYWORDS

Homo sapiens (human)

SOURCE

Homo sapiens

ORGANISM

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

REFERENCE

1 (bases 1 to 560)

Sondermann, P., Huber, R. and Jakob, U.

Recombinant soluble Fc receptors

Patent: JP 2002531086-A 5 24-SEP-2002;

MAX PLANCK GESELLSCHAFT ZUR FÖRDERUNG DER WISSENSCHAFTEN EV

OS

PN JP 2002531086-A/5

PD 24-SEP-2002

PF 03-DEC-1999 JP 2000585398

PR 03-DEC-1998 EP 98122969, 3

PI PETER SONDERMANN, ROBERT HUBER, UWE JAKOB

PC C12N15/09, A61K38/00, A61K45/00, A61P19/02, A61P29/00, A61P31/18, A61P35/00,

PC A61P37/02, A61P37/08, C07K14/735, C12N1/21, G01N33/53, G01N33/53//

PC A61P37/02, C12N1/19, C12N15/00, A61K37/02

CC (C12N1/21, C12R1:19)

CC Description of Artificial Sequence: Primer

CC Description of Artificial Sequence: Primer

PH Key

Location/Qualifiers

1..560

FT source

/organism="Homo sapiens (human)"

FT

Location/Qualifiers

```

source
1..560
/organism="Homo sapiens"
/mol_type="genomic DNA"
/db_xref="taxon:9606"

ORIGIN
Query Match      100.0%; Score 516; DB 6; Length 560;
Best Local Similarity 100.0%; Pred. No. 2.3e-147;
Matches 516; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GTCCCTCAGAACCTAAGGTCCTCTTGAACCTCCATGGAATAGAAATATTTAAAGGAGAG 60
DB 10 GTCCCTCAGAACCTAAGGTCCTCTTGAACCTCCATGGAATAGAAATATTTAAAGGAGAG 69

QY 61 AATGTGACTCTTACATGTAATGGGAACAATTTCTTTTGAAGTCAGTTCCACCACCAATGTTTC 120
DB 70 AATGTGACTCTTACATGTAATGGGAACAATTTCTTTTGAAGTCAGTTCCACCACCAATGTTTC 129

QY 121 CACAATGGCAGCCCTTTCAGAGAGACAAATTCAGATTTGAATATTTGTGAATGCCAAATTT 180
DB 130 CACAATGGCAGCCCTTTCAGAGAGACAAATTCAGATTTGAATATTTGTGAATGCCAAATTT 189

QY 181 GAAGACAGTGGAGAAATACAAATGTCAGACCAACAAGTTAATGAGAGTGAACCTGTGTAC 240
DB 190 GAAGACAGTGGAGAAATACAAATGTCAGACCAACAAGTTAATGAGAGTGAACCTGTGTAC 249

QY 241 CTGGAAGTCTTTCAGTGAAGTCTCTCTTTCAGGCTCTCTGCTGAGGTGGTGAAGGGC 300
DB 250 CTGGAAGTCTTTCAGTGAAGTCTCTCTTTCAGGCTCTCTGCTGAGGTGGTGAAGGGC 309

QY 301 CAGCCCTCTTCTCAGTGGCCATGTTGGAGGAACCTGGGATGTACAGGTGATCTAT 360
DB 310 CAGCCCTCTTCTCAGTGGCCATGTTGGAGGAACCTGGGATGTACAGGTGATCTAT 369

QY 361 TATAAGGATGGTGAAGTCTCAAGTACTGTGTATGAGAACCAACAATCTCCATTACAAAT 420
DB 370 TATAAGGATGGTGAAGTCTCAAGTACTGTGTATGAGAACCAACAATCTCCATTACAAAT 429

QY 421 GCCACAGTTGAAGACAGTGGAACTACTACTGTACGGGCAAGTGTGGCAGCTGACTAT 480
DB 430 GCCACAGTTGAAGACAGTGGAACTACTACTGTACGGGCAAGTGTGGCAGCTGACTAT 489

QY 481 GAGTCTGAGCCCTCAACATTACTGTATAAAGCT 516
DB 490 GAGTCTGAGCCCTCAACATTACTGTATAAAGCT 525

RESULT 6
AX026805
LOCUS
DEFINITION
Sequence 11 from Patent EP1006183.
ACCESSION
AX026805
VERSION
AX026805.1 GI:10187938
KEYWORDS
SOURCE
Homo sapiens (human)
ORGANISM
Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1
REFERENCE
AUTHORS
TITLE
Recombinant soluble fc receptors
JOURNAL
Patent: EP 1006183-A 11 07-JUN-2000;
MAX PLANCK GESELLSCHAFT (DE)
FEATURES
source
1..560
/organism="Homo sapiens"
/mol_type="unassigned DNA"
/db_xref="taxon:9606"

ORIGIN
Query Match      100.0%; Score 516; DB 6; Length 560;
Best Local Similarity 100.0%; Pred. No. 2.3e-147;
Matches 516; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GTCCCTCAGAACCTAAGGTCCTCTTGAACCTCCATGGAATAGAAATATTTAAAGGAGAG 60
DB 10 GTCCCTCAGAACCTAAGGTCCTCTTGAACCTCCATGGAATAGAAATATTTAAAGGAGAG 69

QY 61 AATGTGACTCTTACATGTAATGGGAACAATTTCTTTTGAAGTCAGTTCCACCACCAATGTTTC 120
DB 70 AATGTGACTCTTACATGTAATGGGAACAATTTCTTTTGAAGTCAGTTCCACCACCAATGTTTC 129

QY 121 CACAATGGCAGCCCTTTCAGAGAGACAAATTCAGATTTGAATATTTGTGAATGCCAAATTT 180
DB 130 CACAATGGCAGCCCTTTCAGAGAGACAAATTCAGATTTGAATATTTGTGAATGCCAAATTT 189

QY 181 GAAGACAGTGGAGAAATACAAATGTCAGACCAACAAGTTAATGAGAGTGAACCTGTGTAC 240
DB 190 GAAGACAGTGGAGAAATACAAATGTCAGACCAACAAGTTAATGAGAGTGAACCTGTGTAC 249

QY 241 CTGGAAGTCTTTCAGTGAAGTCTCTCTTTCAGGCTCTCTGCTGAGGTGGTGAAGGGC 300
DB 250 CTGGAAGTCTTTCAGTGAAGTCTCTCTTTCAGGCTCTCTGCTGAGGTGGTGAAGGGC 309

QY 301 CAGCCCTCTTCTCAGTGGCCATGTTGGAGGAACCTGGGATGTACAGGTGATCTAT 360
DB 310 CAGCCCTCTTCTCAGTGGCCATGTTGGAGGAACCTGGGATGTACAGGTGATCTAT 369

QY 361 TATAAGGATGGTGAAGTCTCAAGTACTGTGTATGAGAACCAACAATCTCCATTACAAAT 420
DB 370 TATAAGGATGGTGAAGTCTCAAGTACTGTGTATGAGAACCAACAATCTCCATTACAAAT 429

QY 421 GCCACAGTTGAAGACAGTGGAACTACTACTGTACGGGCAAGTGTGGCAGCTGACTAT 480
DB 430 GCCACAGTTGAAGACAGTGGAACTACTACTGTACGGGCAAGTGTGGCAGCTGACTAT 489

QY 481 GAGTCTGAGCCCTCAACATTACTGTATAAAGCT 516
DB 490 GAGTCTGAGCCCTCAACATTACTGTATAAAGCT 525

RESULT 7
AX175486
LOCUS
DEFINITION
Sequence 10 from patent US 6309832.
ACCESSION
AX175486
VERSION
AX175486.1 GI:17916785
KEYWORDS
SOURCE
Unknown.
ORGANISM
Unclassified.
REFERENCE
1 (bases 1 to 591)
AUTHORS
Frank G.R., Porter J.P., Rushlow, K.E. and Wassom, D.L.
TITLE
Method to detect IGE
JOURNAL
Patent: US 6309832-A 10 30-OCT-2001;
FEATURES
source
1..591
/organism="unknown"
/mol_type="unassigned DNA"

ORIGIN
Query Match      100.0%; Score 516; DB 6; Length 591;
Best Local Similarity 100.0%; Pred. No. 2.3e-147;
Matches 516; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GTCCCTCAGAACCTAAGGTCCTCTTGAACCTCCATGGAATAGAAATATTTAAAGGAGAG 60
DB 76 GTCCCTCAGAACCTAAGGTCCTCTTGAACCTCCATGGAATAGAAATATTTAAAGGAGAG 135

QY 61 AATGTGACTCTTACATGTAATGGGAACAATTTCTTTTGAAGTCAGTTCCACCACCAATGTTTC 120
DB 136 AATGTGACTCTTACATGTAATGGGAACAATTTCTTTTGAAGTCAGTTCCACCACCAATGTTTC 195

QY 121 CACAATGGCAGCCCTTTCAGAGAGACAAATTCAGATTTGAATATTTGTGAATGCCAAATTT 180
DB 196 CACAATGGCAGCCCTTTCAGAGAGACAAATTCAGATTTGAATATTTGTGAATGCCAAATTT 255

```

Qy	181	GAAGACAGTGGAGAAATACAAATGTGACGACCAACAGATTTAATGAGAGTGAACCTGTGTAC	240
Db	256	GAAGACAGTGGAGAAATACAAATGTGACGACCAACAGATTTAATGAGAGTGAACCTGTGTAC	315
Qy	241	CTGGAAGTCTTTCAGTGACTGGCTGCTCCTTCAGGCTCTGCTGAGTGTGATGGAGGCG	300
Db	316	CTGGAAGTCTTTCAGTGACTGGCTGCTCCTTCAGGCTCTGCTGAGTGTGATGGAGGCG	375
Qy	301	CAGCCCCCTTCTCAGTGGCCATGGTGTGGAGAACTGGGATGTGTACAAGTGTATCTAT	360
Db	376	CAGCCCCCTTCTCAGTGGCCATGGTGTGGAGAACTGGGATGTGTACAAGTGTATCTAT	435
Qy	361	TATAGGATGGTGAAGCTCTCAAGTACTGTTATGAGAACCAACAACATCTCCATTACAAT	420
Db	436	TATAGGATGGTGAAGCTCTCAAGTACTGTTATGAGAACCAACAACATCTCCATTACAAT	495
Qy	421	GCACAGTTGAAGACAGTGGAACTTACTACTGACGGGAAAGTGTGGCAGCTGGACTAT	480
Db	496	GCACAGTTGAAGACAGTGGAACTTACTACTGACGGGAAAGTGTGGCAGCTGGACTAT	555
Qy	481	GAGTCTGAGCCCTCAACATTACTGTAATAAAGCT	516
Db	556	GAGTCTGAGCCCTCAACATTACTGTAATAAAGCT	591
RESULT 8			
AX074293			
LOCUS	AX074293	Sequence 7 from Patent WO0104310.	591 bp DNA linear PAT 06-FEB-2001
DEFINITION	AX074293		
ACCESSION	AX074293.1	GI:12710480	
VERSION			
KEYWORDS			
SOURCE			
ORGANISM			
		Homo sapiens (human)	
		Homo sapiens	
		Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;	
		Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.	
REFERENCE			
AUTHORS		Weber, E.R., Wood, K.V. and Hall, M.P.	
TITLE		Fc epsilon receptor-luminescence inducing protein chimeric nucleic acid molecules, fusion proteins and uses thereof	
JOURNAL		Patent: WO 0104310-A 7 18-JAN-2001;	
		Heska Corporation (US) ; PROMEGA CORPORATION (US)	
FEATURES			
source		1..591	
		/organism="Homo sapiens"	
		/mol_type="unassigned DNA"	
		/db_xref="taxon:9606"	
CDS		1..>591	
		/note="unnamed protein product"	
		/codon_start=1	
		/protein_id="CAC28465.1"	
		/db_xref="GI:12710481"	
		/db_xref="REMBL:CAC28465"	
		/translation="MAFAMESPILLCLVALLFFAPDGVLAVPQKPVSLNPPNRIKPG ENVLTGNMNFVSSTAVFHNGSLSEETNSLNINAKFEDSGEYKCOHQVNSE PVYLEVDMLLQGAASVYVQKQPLFLRCHGRNWDYKVIYYKDGEALKYVYENHN ISITNATVEDSGTYTCTGKWQVLDSEPLNITVKA"	
ORIGIN			
		Query Match 100.0%; Score 516; DB 6; Length 591;	
		Best Local Similarity 100.0%; Pred. No. 2.3e-147;	
		Matches 516; Conservative 0; Mismatches 0; Indels 0; Gaps 0;	
Qy	1	GTCCCTCAGAAACCTTAAGGTCCTCTTGAACCCCTCCATGGAATAGATAATTTAAAGGAGAG	60
Db	76	GTCCCTCAGAAACCTTAAGGTCCTCTTGAACCCCTCCATGGAATAGATAATTTAAAGGAGAG	135
Qy	61	AATGTGACTCTTACATGTAAATGGGAAACAATTTCTTTGAAGTCAGTTCACCAAAATGGTTC	120
Db	136	AATGTGACTCTTACATGTAAATGGGAAACAATTTCTTTGAAGTCAGTTCACCAAAATGGTTC	195
Qy	121	CACAATGGCAGCCCTTTCAGAAAGACAAAATTCGAATTTCAAGTTTCAATATTGTGAATGCCAAATTT	180

```

Db      276 CTGGAAGTCTTCAGTGACTGGCTGCTCTCTCAGGCTCTGCTGAGGTGGTATGAGGGC 217
QY      301 CAGCCCTCTTCTCAGTGAGTGGCTGCTCTCAGGCTCTGCTGAGGTGGTATGAGGGC 360
Db      216 CAGCCCTCTTCTCAGTGAGTGGCTGCTCTCAGGCTCTGCTGAGGTGGTATGAGGGC 157
QY      361 TATAAGGATGGTGAAGCTCTCAAGTACTGGTATGAGAACCAACAATCTCCATTACAAAT 420
Db      156 TATAAGGATGGTGAAGCTCTCAAGTACTGGTATGAGAACCAACAATCTCCATTACAAAT 97
QY      421 GCCCAGTTGAAGACAGTGGAACTTACTACTGTCAGGCAAGGTGGCAGCTGGACTAT 480
Db      96 GCCCAGTTGAAGACAGTGGAACTTACTACTGTCAGGCAAGGTGGCAGCTGGACTAT 37
QY      481 GAGTCTGAGCCCTCAACATTACTGTATAAAAGCT 516
Db      36 GAGTCTGAGCCCTCAACATTACTGTATAAAAGCT 1

RESULT 10
AX074290
LOCUS      AX074290          696 bp      DNA      linear      PAT 06-FEB-2001
DEFINITION Sequence 4 from Patent WO0104310.
ACCESSION  AX074290
VERSION     AX074290.1  GI:12710477
KEYWORDS   Homo sapiens (human)
SOURCE     Homo sapiens
ORGANISM   Homo sapiens

REFERENCE
AUTHORS    Weber,E.R., Wood,K.V. and Hall,M.P.
TITLE      Fc epsilon receptor-luminescence inducing protein chimeric nucleic
JOURNAL    acid molecules, fusion proteins and uses thereof
PATENT:    WO 0104310-A 4 18-JAN-2001;
Heska Corporation (US) ; PROMEGA CORPORATION (US)
FEATURES   source
            1..696
            /organism="Homo sapiens"
            /mol_type="unassigned DNA"
            /db_xref="taxon:9606"
            <1..5696
            /note="unnamed protein product"
            /codon_start=1
            /protein_id="CAC28464.1"
            /db_xref="GI:12710478"
            /db_xref="RENTREMBL:CAC28464"
            /translation="VQPKPKVSLNPPNRI PKGENTVLTGNGNPFVSSTKWFNGS
LSEETNSLNINAKEDSEYKQCHQVNESEPVLYFVSDMLLQASAEVVMGQD
LFLRCHGWRNDYVIYKDGKALYENHNISITNATVEDSGTYTCTGVKWDYD
ESEPLNITIKAPREKYLQFPIPLLVILFAVDITGLFISTQQQVTFLLKIKRTRKG
RLNPPKPNPKGN"

CDS
Query Match      100.0%; Score 516; DB 6; Length 696;
Best Local Similarity 100.0%; Pred. No. 2.4e-147;
Matches 516; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1  GTCCCTCAGAACTAAGTCTCTTGAACCTCCATGGAATAGATATTTAAAGGAGAG 60
Db      1  GTCCCTCAGAACTAAGTCTCTTGAACCTCCATGGAATAGATATTTAAAGGAGAG 60
QY      61  AATGTGACTCTTACATGTAATGGGAACAATTTCTTTGAAGTCAGTTCACCAAAATGGTTC 120
Db      61  AATGTGACTCTTACATGTAATGGGAACAATTTCTTTGAAGTCAGTTCACCAAAATGGTTC 120
QY      121  CACAATGGGAGCCTTTTCAGAGAGACAATTCAGTTTCAATATTTGAATGCCAAATTT 180
Db      121  CACAATGGGAGCCTTTTCAGAGAGACAATTCAGTTTCAATATTTGAATGCCAAATTT 180
QY      181  GAAGACAGTGGAGAATACAAATGTGAGCAACCAAGTTAATGAGAGTGAACCTGTGTAC 240

```

```

Db      181 GAAGACAGTGGAGAATACAAATGTGAGCAACCAAGTTAATGAGAGTGAACCTGTGTAC 240
QY      241  CTGGAAGTCTTCAGTGACTGGCTGCTCTCAGGCTCTGCTGAGGTGGTATGAGGGC 300
Db      241  CTGGAAGTCTTCAGTGACTGGCTGCTCTCAGGCTCTGCTGAGGTGGTATGAGGGC 300
QY      301  CAGCCCTCTTCTCAGTGAGTGGCTGCTCTCAGGCTCTGCTGAGGTGGTATGAGGGC 360
Db      301  CAGCCCTCTTCTCAGTGAGTGGCTGCTCTCAGGCTCTGCTGAGGTGGTATGAGGGC 360
QY      361  TATAAGGATGGTGAAGCTCTCAAGTACTGGTATGAGAACCAACAATCTCCATTACAAAT 420
Db      361  TATAAGGATGGTGAAGCTCTCAAGTACTGGTATGAGAACCAACAATCTCCATTACAAAT 420
QY      421  GCCCAGTTGAAGACAGTGGAACTTACTACTGTCAGGCAAGGTGGCAGCTGGACTAT 480
Db      421  GCCCAGTTGAAGACAGTGGAACTTACTACTGTCAGGCAAGGTGGCAGCTGGACTAT 480
QY      481  GAGTCTGAGCCCTCAACATTACTGTATAAAAGCT 516
Db      481  GAGTCTGAGCCCTCAACATTACTGTATAAAAGCT 516

RESULT 11
AX074292/c
LOCUS      AX074292          596 bp      DNA      linear      PAT 06-FEB-2001
DEFINITION Sequence 6 from Patent WO0104310.
ACCESSION  AX074292
VERSION     AX074292.1  GI:12710479
KEYWORDS   Homo sapiens (human)
SOURCE     Homo sapiens
ORGANISM   Homo sapiens

REFERENCE
AUTHORS    Weber,E.R., Wood,K.V. and Hall,M.P.
TITLE      Fc epsilon receptor-luminescence inducing protein chimeric nucleic
JOURNAL    acid molecules, fusion proteins and uses thereof
PATENT:    WO 0104310-A 6 18-JAN-2001;
Heska Corporation (US) ; PROMEGA CORPORATION (US)
FEATURES   source
            1..696
            /organism="Homo sapiens"
            /mol_type="unassigned DNA"
            /db_xref="taxon:9606"

ORIGIN
Query Match      100.0%; Score 516; DB 6; Length 696;
Best Local Similarity 100.0%; Pred. No. 2.4e-147;
Matches 516; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1  GTCCCTCAGAACTAAGTCTCTTGAACCTCCATGGAATAGATATTTAAAGGAGAG 60
Db      596  GTCCCTCAGAACTAAGTCTCTTGAACCTCCATGGAATAGATATTTAAAGGAGAG 637
QY      61  AATGTGACTCTTACATGTAATGGGAACAATTTCTTTGAAGTCAGTTCACCAAAATGGTTC 120
Db      636  AATGTGACTCTTACATGTAATGGGAACAATTTCTTTGAAGTCAGTTCACCAAAATGGTTC 577
QY      121  CACAATGGGAGCCTTTTCAGAGAGACAATTCAGTTTCAATATTTGAATGCCAAATTT 180
Db      576  CACAATGGGAGCCTTTTCAGAGAGACAATTCAGTTTCAATATTTGAATGCCAAATTT 517
QY      181  GAAGACAGTGGAGAATACAAATGTGAGCAACCAAGTTAATGAGAGTGAACCTGTGTAC 240
Db      516  GAAGACAGTGGAGAATACAAATGTGAGCAACCAAGTTAATGAGAGTGAACCTGTGTAC 457
QY      241  CTGGAAGTCTTCAGTGACTGGCTGCTCTCAGGCTCTGCTGAGGTGGTATGAGGGC 300
Db      456  CTGGAAGTCTTCAGTGACTGGCTGCTCTCAGGCTCTGCTGAGGTGGTATGAGGGC 397
QY      301  CAGCCCTCTTCTCAGTGAGTGGCTGCTCTCAGGCTCTGCTGAGGTGGTATGAGGGC 360

```

Db 396 CAGCCCTCTTCTCAGGTGCCATCGTTGGAGAACTGGGTGTGTACAAGGTGATCTAT 337
Qy 361 TATAGGATGGTGAAGCTCTCAAGTACTGGTATGAGAACCAACATCTCCATTACAAAT 420
Db 336 TATAGGATGGTGAAGCTCTCAAGTACTGGTATGAGAACCAACATCTCCATTACAAAT 277
Qy 421 GCCACAGTTGAAGACAGTGGAACTTACTACTCTACGGCAAGTGTGGCAGCTGGACTAT 480
Db 276 GCCACAGTTGAAGACAGTGGAACTTACTACTCTACGGCAAGTGTGGCAGCTGGACTAT 217
Qy 481 GAGTCTGAGCCCTCAACATTACTGTATAAAGCT 516
Db 216 GAGTCTGAGCCCTCAACATTACTGTATAAAGCT 181

RESULT 12
AR175483
LOCUS AR175483 699 bp DNA linear PAT 17-DEC-2001
DEFINITION Sequence 7 from patent US 6309832.
ACCESSION AR175483
VERSION AR175483.1 GI:17916782
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE
AUTHORS Frank, G.R., Porter, J.P., Rushlow, K.E. and Wasson, D.L.
TITLE Method to detect Ige
JOURNAL Patent: US 6309832-A 7 30-OCT-2001;
FEATURES
source 1..699
/organism="unknown"
/mol_type="unassigned DNA"

ORIGIN
Query Match 100.0%; Score 516; DB 6; Length 699;
Best Local Similarity 100.0%; Pred. No. 2.4e-147;
Matches 516; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GTCCTCAGAAACCTAAGGTCTCTTGAACCCCTCCATGGAATAGATATTTAAAGAGAG 60
Db 1 GTCCTCAGAAACCTAAGGTCTCTTGAACCCCTCCATGGAATAGATATTTAAAGAGAG 60
Qy 61 AATGTGACTCTTACATGTATGGAACAATTTCTTTGAAGTCAAGTTCCACCAATGGTTC 120
Db 61 AATGTGACTCTTACATGTATGGAACAATTTCTTTGAAGTCAAGTTCCACCAATGGTTC 120
Qy 121 CACAATGGCAGCCCTTTCAGAAAGACAAATTCAGTTTGAATTTGGAATGCCAAATTT 180
Db 121 CACAATGGCAGCCCTTTCAGAAAGACAAATTCAGTTTGAATTTGGAATGCCAAATTT 180
Qy 181 GAAGACAGTGGAGATACAAATGTCAGACCAACAGTTTAAATGAGAGTGAACCTGTGAC 240
Db 181 GAAGACAGTGGAGATACAAATGTCAGACCAACAGTTTAAATGAGAGTGAACCTGTGAC 240
Qy 241 CTGGAAGTCTTCAAGTACTGGCTCTCTTCAGGCCCTCTCTGAGGTGGTGTGAGGGGC 300
Db 241 CTGGAAGTCTTCAAGTACTGGCTCTCTTCAGGCCCTCTCTGAGGTGGTGTGAGGGGC 300
Qy 301 CAGCCCTCTTCTCAGGTGCCATGGTGGAGAACCTGGATGTACAGGTGATCTAT 360
Db 301 CAGCCCTCTTCTCAGGTGCCATGGTGGAGAACCTGGATGTGTAACAAGGTGATCTAT 360
Qy 361 TATAGGATGGTGAAGCTCTCAAGTACTGGTATGAGAACCAACATCTCCATTACAAAT 420
Db 361 TATAGGATGGTGAAGCTCTCAAGTACTGGTATGAGAACCAACATCTCCATTACAAAT 420
Qy 421 GCCACAGTTGAAGACAGTGGAACTTACTACTCTACGGGCAAGTGTGGCAGCTGGACTAT 480
Db 421 GCCACAGTTGAAGACAGTGGAACTTACTACTCTACGGGCAAGTGTGGCAGCTGGACTAT 480
Qy 481 GAGTCTGAGCCCTCAACATTACTGTATAAAGCT 516

Db 481 GAGTCTGAGCCCTCAACATTACTGTATAAAGCT 516

RESULT 13
E07699
LOCUS E07699 713 bp RNA linear PAT 29-SEP-1997
DEFINITION cDNA encoding human soluble Fc epsilon RI alpha chain.
ACCESSION E07699.1 GI:2175833
VERSION JP 1994169776-A/1.
KEYWORDS Homo sapiens (human)
SOURCE Homo sapiens
ORGANISM Homo sapiens
REFERENCE
AUTHORS Ra, T., Naito, Y. and Hirama, M.
TITLE PRODUCTION OF SOLUBLE HUMAN FcEPSILONRIALPHA CHAIN
JOURNAL Patent: JP 1994169776-A 1 21-JUN-1994;
COMMENT RA TOMOYASU, GREEN CROSS CORP:THE
OS Homo sapiens (human)
PN JP 1994169776-A/1
PD 21-JUN-1994
PF 29-JUL-1993 JP 1993208217
PR 04-AUG-1992 JP 92P 229227
PI RA TOMOYASU, NAITO YUKITSUGU, HIRAMA MINORU
PC C12N15/13, C12N5/10, C12P21/02;
CC strandedness: Double;
CC topology: Linear;
CC hypothetical: No;
CC anti-sense: No;
FH Key Location/Qualifiers
FT 1..713
FT /organism='Homo sapiens'
FT /cell_type='basophils precursor cell' FT
FT /cell_lines='KU812'
FT /clone='Fc epsilon RI/pM1'
FT mat_peptide 120..710
FT /product='human soluble Fc epsilon RI alpha chain'.
FEATURES
source 1..713
/organism='Homo sapiens'
/mol_type='genomic RNA'
/db_xref='taxon:9606'

ORIGIN
Query Match 100.0%; Score 516; DB 6; Length 713;
Best Local Similarity 100.0%; Pred. No. 2.4e-147;
Matches 516; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GTCCCTCAGAAACCTAAGGTCTCTTGAACCCCTCCATGGAATAGATATTTAAAGAGAG 60
Db 195 GTCCCTCAGAAACCTAAGGTCTCTTGAACCCCTCCATGGAATAGATATTTAAAGAGAG 254
Qy 61 AATGTGACTCTTACATGTATGGAACAATTTCTTTGAAGTCAAGTTCCACCAATGGTTC 120
Db 255 AATGTGACTCTTACATGTATGGAACAATTTCTTTGAAGTCAAGTTCCACCAATGGTTC 314
Qy 121 CACAATGGCAGCCCTTTCAGAAAGACAAATTCAGTTTGAATTTGGAATGCCAAATTT 180
Db 315 CACAATGGCAGCCCTTTCAGAAAGACAAATTCAGTTTGAATTTGGAATGCCAAATTT 374
Qy 181 GAAGACAGTGGAGATACAAATGTCAGACCAACAGTTTAAATGAGAGTGAACCTGTGAC 240
Db 375 GAAGACAGTGGAGATACAAATGTCAGACCAACAGTTTAAATGAGAGTGAACCTGTGAC 434
Qy 241 CTGGAAGTCTTCAAGTACTGGCTCTCTTCAGGCCCTCTCTGAGGTGGTGTGAGGGGC 300
Db 435 CTGGAAGTCTTCAAGTACTGGCTCTCTTCAGGCCCTCTCTGAGGTGGTGTGAGGGGC 494
Qy 301 CAGCCCTCTTCTCAGGTGCCATGGTGGAGAACCTGGATGTGTAACAAGGTGATCTAT 360

GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.

OM nucleic - nucleic search, using sw model

Run on: October 8, 2004, 15:03:47 ; Search time 250.898 Seconds
(without alignments)
8736.904 Million cell updates/sec

Title: US-10-763-400-12
Perfect score: 516
Sequence: 1 gcccttcgaaacctaaagt.....acattactgtaataaaagct 516

Scoring table: IDENTITY NUC
Gapop 10.0 , Gapext 1.0

Searched: 3373863 seqs, 2124095041 residues

Total number of hits satisfying chosen parameters: 6747726

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : N Geneseq_29Jan04:.*
1: geneseqn1980s:.*
2: geneseqn1990s:.*
3: geneseqn2000s:.*
4: geneseqn2001as:.*
5: geneseqn2001bs:.*
6: geneseqn2002s:.*
7: geneseqn2003as:.*
8: geneseqn2003bs:.*
9: geneseqn2003cs:.*
10: geneseqn2004s:.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	516	100.0	516	3	AAA27302 Human nhf
2	516	100.0	516	5	Aaf24917 DNA encod
3	516	100.0	516	5	Aaf24918 Complemen
4	516	100.0	528	3	AAA27301 Human Fce
5	516	100.0	528	4	Aah47768 Nucleotid
6	516	100.0	570	3	AAA27472 Recombina
7	516	100.0	591	5	Aaf24916 Complemen
8	516	100.0	591	5	Aaf24915 DNA encod
9	516	100.0	696	5	Aaf24914 Complemen
10	516	100.0	696	5	Aaf24913 Nucleotid
11	516	100.0	713	2	Aaq55969 Human dii
12	516	100.0	773	2	Aav20402 Human IGE
13	516	100.0	773	6	Abss2959 Human cdn
14	516	100.0	774	4	Aaf97964 Human imm
15	516	100.0	851	2	Aaq27267 Human fce
16	516	100.0	898	8	Acd06182 Human cdn
17	516	100.0	1068	3	AAA27470 Human fce
18	516	100.0	1088	1	Aan90126 cDNA enco
19	516	100.0	1174	2	Aaf51020 Human fce
20	516	100.0	1197	2	Aat85615 Alpha sub
21	516	100.0	1198	2	Aav36343 cDNA enco
22	516	100.0	1198	3	AAA34813 Human ade
23	516	100.0	1198	3	Aaf20935 Human hig

24	516	100.0	1198	4	AAF77692 Human wil
25	516	100.0	1198	5	AAF24912 Complemen
26	516	100.0	1198	5	AAF24911 Nucleotid
27	516	100.0	1198	6	ABL67793 Oesophagu
28	516	100.0	1198	7	ABZ96629 Human hig
29	516	100.0	1198	9	ADB85535 Human imm
30	516	100.0	1908	5	AAF24929 Fc epsilo
31	516	100.0	1908	5	AAF24928 Fc epsilo
32	516	100.0	1983	5	AAF24927 Fc epsilo
33	516	100.0	2193	5	AAF24926 Complemen
34	516	100.0	2193	5	AAF24923 Complemen
35	516	100.0	2268	5	AAF24921 Complemen
36	516	100.0	2268	5	AAF24920 Nucleotid
37	516	100.0	2955	2	AAV20404 Plasmid R
38	516	100.0	2955	6	ABSS2957 Human cdn
39	516	100.0	21742	3	AAA34816 Human ade
40	516	100.0	21742	3	AAF20938 Human hig
41	516	100.0	21742	7	ABZ96632 Human hig
42	516	100.0	117608	7	ABZ97129 Human rec
43	516	100.0	117609	3	AAF21435 Human rec
44	514.4	99.7	1199	2	AAQ14736 Human Fc(
45	512.8	99.4	1193	2	AAQ04644 Encodes a

ALIGNMENTS

RESULT 1
AAA27302
ID AAA27302 standard; cDNA; 516 BP.
AC
AC AAA27302;
DT 01-AUG-2000 (first entry)
DE Human nhFcpsilonRIalpha 1-516 gene.
KW Protein co-ordinate data; nhFcpsilonRIalpha 1-516; FcR;
KW FcpsilonRIalpha 1-516; antibody Fc receptor; allergy;
KW anaphylactic shock; ss.
CS Homo sapiens.
FH Key Location/Qualifiers
FT CDS 1..516
FT /tag= a
FT /product= "nhFcpsilonRIalpha 1-516"
FT /partial
XX WO200026246-A2.
XX 11-MAY-2000.
XX 05-NOV-1999; 99WO-US026203.
XX 05-NOV-1999; 98US-0107219P.
XX (HESK-) HESKA CORP.
XX (NOUN) UNIV NORTHWESTERN.
XX Jaretzky TS, Garman SC, Kinet J;
XX WPI; 2000-365577/31.
XX P-PSDB; AAY94211.
XX Three-dimensional model comprising an extracellular domain of a human
XX high affinity Fc epsilon receptor alpha chain protein, useful for
XX identifying inhibitors and useful mutains.
XX Example 6; Page 461; 463pp; English.
XX The present sequence is the human FcpsilonRIalpha 1-516 gene (also known
XX as nhFcpsilonRIalpha 1-516). Along with either the FcpsilonRI beta

CC and/or gamma subunits, the protein produced from this gene is involved in
 CC mast cell activation and the triggering of allergic reactions and
 CC anaphylactic shock. The protein can be used to identify useful mutants
 CC and inhibitors, which can then be used in the detection of
 CC (susceptibility to) allergies and in protecting animals from these
 CC allergies

SQ Sequence 516 BP; 155 A; 107 C; 124 G; 130 T; 0 U; 0 Other;
 Query Match 100.0%; Score 516; DB 3; Length 516;
 Best Local Similarity 100.0%; Pred. No. 2.1e-148; Indels 0; Gaps 0;
 Matches 516; Conservative 0; Mismatches 0;
 QY 1 GTCCCTCAGAACCTTAAGTCTCCTTGAACCTCCATGGAATAGATATTAAAGGAGAG 60
 Db 1 GTCCCTCAGAACCTTAAGTCTCCTTGAACCTCCATGGAATAGATATTAAAGGAGAG 60
 QY 61 AATGTGACTCTACATGTAATGGGACAAATTTCTTGAAGTCAGTTCCACCAATGGTTC 120
 Db 61 AATGTGACTCTACATGTAATGGGACAAATTTCTTGAAGTCAGTTCCACCAATGGTTC 120
 QY 121 CACATGCGAGCCTTTTCAAGAGACAAATTTCAAGTTTGAATTTGGAATGCCAAATTT 180
 Db 121 CACATGCGAGCCTTTTCAAGAGACAAATTTCAAGTTTGAATTTGGAATGCCAAATTT 180
 QY 181 GAAGACAGTGGAGAAATACAAATGTGAGACCAACAAAGTTAATGAGTGAACCTGTGTAC 240
 Db 181 GAAGACAGTGGAGAAATACAAATGTGAGACCAACAAAGTTAATGAGTGAACCTGTGTAC 240
 QY 241 CTGGAAGTCTTCAAGTCTGCTCTCTCAGGCTCTGCTGAGGTGGTGGAGGGC 300
 Db 241 CTGGAAGTCTTCAAGTCTGCTCTCTCAGGCTCTGCTGAGGTGGTGGAGGGC 300
 QY 301 CAGCCCTCTTCTCAGTGCCTAGTGGAGAACTGGGATGTGTAAGGTGAATCTAT 360
 Db 301 CAGCCCTCTTCTCAGTGCCTAGTGGAGAACTGGGATGTGTAAGGTGAATCTAT 360
 QY 361 TATAGGATGTGAAGCTCTCAAGTCTGCTGAGTGGAGAACTGGGATGTGTAAGGTGAAT 420
 Db 361 TATAGGATGTGAAGCTCTCAAGTCTGCTGAGTGGAGAACTGGGATGTGTAAGGTGAAT 420
 QY 421 CCCACAGTTGAAGACAGTGAACCTACTTACTGTACGGGCAAGTGTGGCAGCTGGACTAT 480
 Db 421 CCCACAGTTGAAGACAGTGAACCTACTTACTGTACGGGCAAGTGTGGCAGCTGGACTAT 480
 QY 481 GAGTCTGAGCCCTCAACATTTACTGTATAAAGCT 516
 Db 481 GAGTCTGAGCCCTCAACATTTACTGTATAAAGCT 516

RESULT 2
 AAF24917

ID AAF24917 standard; DNA; 516 BP.

XX AC AAF24917;
 XX DT
 XX DX
 XX DE

30-APR-2001 (first entry)

DNA encoding Fc epsilon receptor alpha-chain secretable protein.

XX Fc epsilon receptor; Fc epsilonR; immunoglobulin E; IgE; atopic disease;
 KW luminescence inducing protein; allergy; hyper IgE syndrome;
 KW internal parasite infection; B cell neoplasia; ss.

XX OS Homo sapiens.

XX PN WO200104310-A1.

XX PD 18-JAN-2001.

XX PF 13-JUL-2000; 2000WO-US019070.

XX PR 13-JUL-1999; 99US-0143612P.

PR 02-MAR-2000; 2000US-0186412P.
 XX (HESK-) HESKA CORP.
 PA (PROM-) PROMEGA CORP.
 XX PI Weber ER, Wood KV, Hall MP;
 XX WI; 2001-103082/11.
 DR P-PSDB; AAB31587.
 XX A fusion protein, comprising an Fc epsilon receptor domain and a
 PT luminescence inducing protein domain that induces a LP substrate to emit
 PT light when contacted with the LP domain, useful for detecting
 PT immunoglobulin (Ig) E.
 XX Claim 17; Page 66-67; 105pp; English.
 CC The present sequence encodes a secretable form of a human Fc epsilon
 CC receptor (Fc epsilonR) alpha-chain. The Fc epsilonR protein binds to
 CC immunoglobulin (Ig) E. The Fc epsilonR domain is used to produce a fusion
 CC protein, which also comprises a luminescence inducing protein domain that
 CC induces a substrate to emit light when contacted with the luminescence
 CC inducing protein domain. The fusion protein may be used to detect IgE. It
 CC may also be used to identify a compound capable of inhibiting Fc epsilonR
 CC protein activity. IgE antibody production is indicative of diseases such
 CC as allergies, atopic disease, hyper IgE syndrome, internal parasite
 CC infections and B cell neoplasia. Detection of IgE production in an animal
 CC following therapy is indicative of the efficacy of the treatment, for
 CC example when using treatments intended to disrupt IgE production
 XX Sequence 516 BP; 155 A; 107 C; 124 G; 130 T; 0 U; 0 Other;
 SQ

Query Match 100.0%; Score 516; DB 5; Length 516;
 Best Local Similarity 100.0%; Pred. No. 2.1e-148;
 Matches 516; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 GTCCCTCAGAACCTTAAGTCTCCTTGAACCTCCATGGAATAGATATTAAAGGAGAG 60
 Db 1 GTCCCTCAGAACCTTAAGTCTCCTTGAACCTCCATGGAATAGATATTAAAGGAGAG 60
 QY 61 AATGTGACTCTTACATGTAATGGGACAAATTTCTTGAAGTCAGTTCCACCAATGGTTC 120
 Db 61 AATGTGACTCTTACATGTAATGGGACAAATTTCTTGAAGTCAGTTCCACCAATGGTTC 120
 QY 121 CACATGCGAGCCTTTTCAAGAGACAAATTTCAAGTTTGAATTTGGAATGCCAAATTT 180
 Db 121 CACATGCGAGCCTTTTCAAGAGACAAATTTCAAGTTTGAATTTGGAATGCCAAATTT 180
 QY 181 GAAGACAGTGGAGAAATACAAATGTGAGACCAACAAAGTTAATGAGTGAACCTGTGTAC 240
 Db 181 GAAGACAGTGGAGAAATACAAATGTGAGACCAACAAAGTTAATGAGTGAACCTGTGTAC 240
 QY 241 CTGGAAGTCTTCAAGTCTGCTCTCTCAGGCTCTGCTGAGGTGGTGGAGGGC 300
 Db 241 CTGGAAGTCTTCAAGTCTGCTCTCTCAGGCTCTGCTGAGGTGGTGGAGGGC 300
 QY 301 CAGCCCTCTTCTCAGTGCCTAGTGGAGAACTGGGATGTGTAAGGTGAATCTAT 360
 Db 301 CAGCCCTCTTCTCAGTGCCTAGTGGAGAACTGGGATGTGTAAGGTGAATCTAT 360
 QY 361 TATAGGATGTGAAGCTCTCAAGTCTGCTGAGTGGAGAACTGGGATGTGTAAGGTGAAT 420
 Db 361 TATAGGATGTGAAGCTCTCAAGTCTGCTGAGTGGAGAACTGGGATGTGTAAGGTGAAT 420
 QY 421 CCCACAGTTGAAGACAGTGAACCTACTTACTGTACGGGCAAGTGTGGCAGCTGGACTAT 480
 Db 421 CCCACAGTTGAAGACAGTGAACCTACTTACTGTACGGGCAAGTGTGGCAGCTGGACTAT 480
 QY 481 GAGTCTGAGCCCTCAACATTTACTGTATAAAGCT 516
 Db 481 GAGTCTGAGCCCTCAACATTTACTGTATAAAGCT 516

RESULT 3		
AA24918/c	AAF24918 standard; DNA; 516 BP.	
ID	AAF24918	
XX		
AC	AAF24918;	
XX		
DT	30-APR-2001 (first entry)	
XX		
DE	Complement of Fc epsilon receptor alpha-chain secretable protein DNA.	
XX		
XX	Fc epsilon receptor; Fc epsilonR; immunoglobulin E; IgE; atopic disease;	
KW	luminescence inducing protein; allergy; hyper IgE syndrome;	
KW	internal parasite infection; B cell neoplasia; ss.	
XX		
OS	Homo sapiens.	
XX		
PN	WO200104310-A1.	
XX		
PD	18-JAN-2001.	
XX		
PF	13-JUL-2000; 2000WO-US019070.	
XX		
PR	13-JUL-1999; 99US-0143612P.	
PR	02-MAR-2000; 2000US-0186412P.	
XX		
PA	(HESK-) HESKA CORP.	
PA	(PROM-) PROMEGA CORP.	
XX		
PI	Weber ER, Wood KV, Hall MP;	
XX		
DR	WPI; 2001-103082/11.	
XX		
PT	A fusion protein, comprising an Fc epsilon receptor domain and a	
PT	luminescence inducing protein domain that induces a LP substrate to emit	
PT	light when contacted with the LP domain, useful for detecting	
PT	immunoglobulin (Ig) E.	
XX		
PS	Example; Page 67-68; 105pp; English.	
XX		
CC	The present sequence represents a secretable form of a human Fc epsilon	
CC	receptor (Fc epsilonR) alpha-chain. The Fc epsilonR protein binds to	
CC	immunoglobulin (Ig) E. The Fc epsilonR domain is used to produce a fusion	
CC	protein, which also comprises a luminescence inducing protein domain that	
CC	induces a substrate to emit light when contacted with the luminescence	
CC	inducing protein domain. The fusion protein may be used to detect IgE. It	
CC	may also be used to identify a compound capable of inhibiting Fc epsilonR	
CC	protein activity. IgE antibody production is indicative of diseases such	
CC	as allergies, atopic disease, hyper IgE syndrome, internal parasite	
CC	infections and B cell neoplasia. Detection of IgE production in an animal	
CC	following therapy is indicative of the efficacy of the treatment, for	
CC	example when using treatments intended to disrupt IgE production	
XX		
SQ	Sequence 516 BP; 130 A; 124 C; 107 G; 155 T; 0 U; 0 Other;	
Query Match 100.0%; Score 516; DB 5; Length 516;		
Best Local Similarity 100.0%; Pred. No. 2.1e-148;		
Matches 516; Conservative 0; Mismatches 0; Indels 0; Gaps 0;		
QY	1 GTCCTCAGAAACCTTAGGTCCTCTTGAACCCCTCCATGGGAATAGAAATTTAAAGAGAG 60	
Db	516 GTCCTCAGAAACCTTAGGTCCTCTTGAACCCCTCCATGGGAATAGAAATTTAAAGAGAG 457	
QY	61 AATGTGACTCTTACATGTAATGGGAACAATTTCTTTGAAGTCAGTTCACCAATGGTTC 120	
Db	456 AATGTGACTCTTACATGTAATGGGAACAATTTCTTTGAAGTCAGTTCACCAATGGTTC 397	
QY	121 CACAATGGCAGCCCTTCAGAGACACAAATTTCAAGTTTGAATTTGTAATGCCAATTT 180	
Db	396 CACAATGGCAGCCCTTCAGAGACACAAATTTCAAGTTTGAATTTGTAATGCCAATTT 337	
QY	181 GAAGACAGTGGAGAAATCAAAATGTGACACCAACCAAGTTAATGAGACTGAACCTGTCTAC 240	
Db	336 GAAGACAGTGGAGAAATCAAAATGTGACACCAACCAAGTTAATGAGACTGAACCTGTCTAC 277	

QY	241	CTGGAAGTCTTTCAGTGACTGGCTGCTCCCTTCAGGCTCTGCTGAGGTGGTGGTGGAGGC	300
Db	276	CTGGAAGTCTTTCAGTGACTGGCTGCTCCCTTCAGGCTCTGCTGAGGTGGTGGTGGAGGC	217
QY	301	CAGCCCTCTTCTCAGGTGCCATGTTGGAGAACTGGAGTGTGTACAAAGGTGATCTAT	360
Db	216	CAGCCCTCTTCTCAGGTGCCATGTTGGAGAACTGGAGTGTGTACAAAGGTGATCTAT	157
QY	361	TATAAGGATGGTGAAGCTCTCAAGTACTGTGTATGAGAACCAACAATCTCCATTACAAAT	420
Db	156	TATAAGGATGGTGAAGCTCTCAAGTACTGTGTATGAGAACCAACAATCTCCATTACAAAT	97
QY	421	GCCACAGTTGAAGACAGATGGAACCTACTACTGACGGCAAAAGTGTGGCAGCTGGACTAT	480
Db	96	GCCACAGTTGAAGACAGATGGAACCTACTACTGACGGCAAAAGTGTGGCAGCTGGACTAT	37
QY	481	GAGTCTGAGCCCTCAACATTACTGTAATAAAAAAGCT	516
Db	36	GAGTCTGAGCCCTCAACATTACTGTAATAAAAAAGCT	1

RESULT 4

AAA27301

ID AAA27301 standard; cDNA; 528 BP.

XX

AC AAA27301;

XX

DT 01-AUG-2000 (first entry)

XX

DE Human Fc epsilonR alpha 1-528 gene.

XX

KW Protein co-ordinate data; nhFc epsilonR alpha 1-528;

KW Fc epsilonR alpha 1-528; FcR; antibody Fc receptor; allergy;

KW anaphylactic shock; ss.

XX

OS Homo sapiens.

XX

TH Key

FT CDS

FT 1..528

FT /*tag= a

FT /product= "Fc epsilonR alpha 1-528"

FT /partial

XX

PN WO200026246-A2.

XX

PD 11-MAY-2000.

XX

PF 05-NOV-1999; 99WO-US026203.

XX

PR 05-NOV-1998; 98US-0107219P.

XX

PA (HESK-) HESKA CORP.

PA (NOUN) UNIV NORTHWESTERN.

XX

PI Jardetzky TS, Garman SC, Kinet J;

XX

DR WPI; 2000-365577/31.

DR P-PSDB; AAY94210.

XX

PT Three-dimensional model comprising an extracellular domain of a human

PT high affinity Fc epsilon receptor alpha chain protein, useful for

PT identifying inhibitors and useful mutants.

XX

PS Disclosure; Page 459-460; 463pp; English.

XX

CC The present sequence is the human Fc epsilonR alpha 1-528 gene (also known

CC as nhFc epsilonR alpha 1-528). Along with either the Fc epsilonR beta

CC and/or gamma subunits, the protein produced from this gene is involved in

CC mast cell activation and the triggering of allergic reactions and

CC anaphylactic shock. The protein can be used to identify useful mutants

CC and inhibitors, which can then be used in the detection of

CC (susceptibility to) allergies and in protecting animals from these

CC allergies
SQ Sequence 528 BP; 158 A; 110 C; 129 G; 131 T; 0 U; 0 Other;
Query Match 100.0%; Score 516; DB 3; Length 528;
Best Local Similarity 100.0%; Pred. No. 2.1e-148;
Matches 516; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 GTCCCTCAGAACCTTAAGTCTCTTGAACCTCCATGGAATAGAAATTTAAAGGAGAG 60
Db 1 GTCCCTCAGAACCTTAAGTCTCTTGAACCTCCATGGAATAGAAATTTAAAGGAGAG 60
QY 61 AATGTGACTCTTACATGTAATGGGACAAATTTCTTTGAAGTCAGTTCACCAATGTTTC 120
Db 61 AATGTGACTCTTACATGTAATGGGACAAATTTCTTTGAAGTCAGTTCACCAATGTTTC 120
QY 121 CACAATGGCAGCCCTTTCAGAGAGACAAATTTCAAGTTTGAATTTGGAATGCCAAATTT 180
Db 121 CACAATGGCAGCCCTTTCAGAGAGACAAATTTCAAGTTTGAATTTGGAATGCCAAATTT 180
QY 181 GAAGACAGTGAGATACAAATGTCAGCACCAACAGTTTAATGAGAGTGAACCTGTGTAC 240
Db 181 GAAGACAGTGAGATACAAATGTCAGCACCAACAGTTTAATGAGAGTGAACCTGTGTAC 240
QY 241 CTGGAAGTCTTCACTGAGTGGCTCTCTTCAGGCTCTCTGAGGTGGTGTGGAGGGC 300
Db 241 CTGGAAGTCTTCACTGAGTGGCTCTCTTCAGGCTCTCTGAGGTGGTGTGGAGGGC 300
QY 301 CAGCCCTCTTCTCAGGTGCTGATGGTGGAGGAACCTGGATGTGTACAAAGTGAATCTAT 360
Db 301 CAGCCCTCTTCTCAGGTGCTGATGGTGGAGGAACCTGGATGTGTACAAAGTGAATCTAT 360
QY 361 TATAAGGATGGTGAAGCTCTCAAGTACTGTTGAGGAACTGAGTGAACCTGTGTAC 420
Db 361 TATAAGGATGGTGAAGCTCTCAAGTACTGTTGAGGAACTGAGTGAACCTGTGTAC 420
QY 421 GCCACAGTTGAGACAGTGAACCTACTCTGTCAGCGCAAGTGTGGAGCTGGACTAT 480
Db 421 GCCACAGTTGAGACAGTGAACCTACTCTGTCAGCGCAAGTGTGGAGCTGGACTAT 480
QY 481 GAGTCTGAGCCCTCAACATTTACTGTATAAAGCT 516
Db 481 GAGTCTGAGCCCTCAACATTTACTGTATAAAGCT 516

RESULT 5
AAH47768
ID AAH47768 standard; DNA; 528 BP.
AC AAH47768;
XX
XX
XX 07-JAN-2002 (first entry)
XX
XX
XX Nucleotide sequence of nhFcpsilonRlaphal-528 molecule.
XX
XX Antibody receptor protein; FcpsilonRlapha protein; immunoglobulin; IgE;
XX mu chain; allergy; protein co-ordinate; ds.
XX
XX Homo sapiens.
XX
XX Key Location/Qualifiers
XX CDS 1..528 a
XX /tag= a
XX /product= "FcpsilonRlaphal-176"
XX
XX WO200169253-A2.
XX
XX
XX 20-SEP-2001.
XX
XX
XX 14-MAR-2001; 2001WO-US008588.
XX
XX 15-MAR-2000; 2000US-0189853P.
XX
XX

(HESK-) HESKA CORP.
(NOUN) UNIV NORTHWESTERN.
Jardetzky TS, Garman SC, Wurtzburg BA, Kinet J;
WPI; 2001-511403/70.
P-PSDB; AAG65597.
Three dimensional models of complexes between antibody receptor proteins and antibodies used to identify modulators of antibody/receptor binding.
Disclosure; Page 209-210; 213pp; English.
The invention relates to three dimensional models of complexes between antibody receptor proteins, especially FcpsilonRlapha proteins, and antibodies, especially Fc-Cepsilon3/Cepsilon4 regions of immunoglobulin (Ig) E antibodies. The models are used to identify an inhibitor of the selective binding between a FcpsilonRlapha protein and an IgE antibody. The model identifies crystal contacts between a FcpsilonRlapha protein and an Fc-Cepsilon3/Cepsilon4 region of an IgE antibody. A mutin that binds to an Fc domain of an antibody (the mutin has improved function (improved stability, increased affinity for an Fc domain of an antibody, altered substrate specificity, increased affinity for an Fc domain of an antibody, altered substrate specificity, and increased solubility) compared to a protein comprising a defined amino acid sequence given in the specification) is used: to protect an animal from an allergy; detect an allergy in an animal; and to enhance the performance of an IgE binding assay. The present sequence represents the nucleotide sequence of a nhFcpsilonRlaphal-528 molecule encoding a nhFcpsilonRlaphal-176 protein
SQ Sequence 528 BP; 158 A; 110 C; 129 G; 131 T; 0 U; 0 Other;
Query Match 100.0%; Score 516; DB 4; Length 528;
Best Local Similarity 100.0%; Pred. No. 2.1e-148;
Matches 516; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 GTCCCTCAGAACCTTAAGTCTCTTGAACCTCCATGGAATAGAAATTTAAAGGAGAG 60
Db 1 GTCCCTCAGAACCTTAAGTCTCTTGAACCTCCATGGAATAGAAATTTAAAGGAGAG 60
QY 61 AATGTGACTCTTACATGTAATGGGACAAATTTCTTTGAAGTCAGTTCACCAATGTTTC 120
Db 61 AATGTGACTCTTACATGTAATGGGACAAATTTCTTTGAAGTCAGTTCACCAATGTTTC 120
QY 121 CACAATGGCAGCCCTTTCAGAGAGACAAATTTCAAGTTTGAATTTGGAATGCCAAATTT 180
Db 121 CACAATGGCAGCCCTTTCAGAGAGACAAATTTCAAGTTTGAATTTGGAATGCCAAATTT 180
QY 181 GAAGACAGTGAGATACAAATGTCAGCACCAACAGTTTAATGAGAGTGAACCTGTGTAC 240
Db 181 GAAGACAGTGAGATACAAATGTCAGCACCAACAGTTTAATGAGAGTGAACCTGTGTAC 240
QY 241 CTGGAAGTCTTCACTGAGTGGCTCTCTTCAGGCTCTCTGAGGTGGTGTGGAGGGC 300
Db 241 CTGGAAGTCTTCACTGAGTGGCTCTCTTCAGGCTCTCTGAGGTGGTGTGGAGGGC 300
QY 301 CAGCCCTCTTCTCAGGTGCTGATGGTGGAGGAACCTGGATGTGTACAAAGTGAATCTAT 360
Db 301 CAGCCCTCTTCTCAGGTGCTGATGGTGGAGGAACCTGGATGTGTACAAAGTGAATCTAT 360
QY 361 TATAAGGATGGTGAAGCTCTCAAGTACTGTTGAGGAACTGAGTGAACCTGTGTAC 420
Db 361 TATAAGGATGGTGAAGCTCTCAAGTACTGTTGAGGAACTGAGTGAACCTGTGTAC 420
QY 421 GCCACAGTTGAGACAGTGAACCTACTCTGTCAGCGCAAGTGTGGAGCTGGACTAT 480
Db 421 GCCACAGTTGAGACAGTGAACCTACTCTGTCAGCGCAAGTGTGGAGCTGGACTAT 480
QY 481 GAGTCTGAGCCCTCAACATTTACTGTATAAAGCT 516
Db 481 GAGTCTGAGCCCTCAACATTTACTGTATAAAGCT 516


```

RESULT 9
AAF24914/c
ID AAF24914 standard; DNA; 696 BP.
XX
XX
AC AAF24914;
XX
DT 30-APR-2001 (first entry)
XX
DE Complement sequence of Fc epsilon receptor alpha-chain mature protein.
XX
XX Fc epsilon receptor; FcepsilonR; immunoglobulin E; IgE; atopic disease;
KW luminescence inducing protein; allergy; hyper IgE syndrome;
KW internal parasite infection; B cell neoplasia; ss.
XX
OS Homo sapiens.
XX
XX WO200104310-A1.
XX
XX 18-JAN-2001.
XX
XX 13-JUL-2000; 2000WO-US019070.
XX
XX 13-JUL-1999; 99US-0143612P.
XX
XX 02-MAR-2000; 2000US-0186412P.
XX
XX (HESK-) HESKA CORP.
XX
XX (PROM-) PROMEGA CORP.
XX
XX Weber ER, Wood KV, Hall MP;
XX
XX WPI; 2001-103082/11.
XX
XX A fusion protein, comprising an Fc epsilon receptor domain and a
XX polynucleotide encoding human Fc epsilon receptor (FcepsilonR) alpha-
XX chain mature protein, that binds to immunoglobulin (Ig) E. The
XX FcepsilonR domain is used to produce a fusion protein, which also
XX comprises a luminescence inducing protein domain that induces a substrate
XX to emit light when contacted with the luminescence inducing protein
XX domain. The fusion protein may be used to detect IgE. It may also be used
XX to identify a compound capable of inhibiting FcepsilonR protein activity.
XX IGE antibody production is indicative of diseases such as allergies,
XX atopic disease, hyper IgE syndrome, internal parasite infections and B
XX cell neoplasia. Detection of IGE production in an animal following
XX therapy is indicative of the efficacy of the treatment, for example when
XX using treatments intended to disrupt IgE production
XX
XX SQ Sequence 696 BP; 179 A; 159 C; 150 G; 208 T; 0 U; 0 Other;
XX
Query Match 100.0%; Score 516; DB 5; Length 696;
Best Local Similarity 100.0%; Pred. No. 2.4e-148;
Matches 516; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
QY 1 GTCCTCAGAAACCTAAGGTCCTCTCAACCCCTCCATGGAATAGATATTTAAGGAG 60
DB 696 GTCCTCAGAAACCTAAGGTCCTCTCAACCCCTCCATGGAATAGATATTTAAGGAG 637
XX
QY 61 AATGTACTCTTACATGTAATGGGAACAATTTCTTTGAAGTCAGTTCCACCAATGGTTC 120
DB 636 AATGTACTCTTACATGTAATGGGAACAATTTCTTTGAAGTCAGTTCCACCAATGGTTC 577
XX
QY 121 CACAATGGCAGCCCTTCAGAGAGACAAATTCAGTTTGAATATGTGGAATGCCAAATTT 180
DB 576 CACAATGGCAGCCCTTCAGAGAGACAAATTCAGTTTGAATATGTGGAATGCCAAATTT 517

```

```

QY 181 GAAGACAGTGGAGATACAAATGTCAGCACCAACAAAGTTTAATGAGAGTGAACCTGTGTAC 240
DB 516 GAAGACAGTGGAGATACAAATGTCAGCACCAACAAAGTTTAATGAGAGTGAACCTGTGTAC 457
XX
QY 241 CTGGAAGTCTTCAAGTCAAGTGGCTGCTCTCTCAGGCTCTCTCAGGCTGCTGAGTGGAGGGC 300
DB 456 CTGGAAGTCTTCAAGTCAAGTGGCTGCTCTCTCAGGCTCTCTCAGGCTGCTGAGTGGAGGGC 397
XX
QY 301 CAGCCCTCTCTCTCAGGTCCTCATGTTGGAGAACTGGGATGTGTACAAGGTGATCTAT 360
DB 396 CAGCCCTCTCTCTCAGGTCCTCATGTTGGAGAACTGGGATGTGTACAAGGTGATCTAT 337
XX
QY 361 TATAAGGATGGTGAAGCTCTCAAGTCAAGTGGTATGAGAACCAACATCTCCATACAAAT 420
DB 336 TATAAGGATGGTGAAGCTCTCAAGTCAAGTGGTATGAGAACCAACATCTCCATACAAAT 277
XX
QY 421 GCCACAGTTGAAGACAGTGGAACTCTACTGTACGGGAAAGTGTGGCAGCTGGACTAT 480
DB 276 GCCACAGTTGAAGACAGTGGAACTCTACTGTACGGGAAAGTGTGGCAGCTGGACTAT 217
XX
QY 481 GAGTCTGAGCCCTCAACATTACTGTATAATAAAGCT 516
DB 216 GAGTCTGAGCCCTCAACATTACTGTATAATAAAGCT 181
XX
RESULT 10
AAF24913
ID AAF24913 standard; DNA; 696 BP.
XX
XX
AC AAF24913;
XX
DT 30-APR-2001 (first entry)
XX
DE Nucleotide sequence of Fc epsilon receptor alpha-chain mature protein.
XX
XX Fc epsilon receptor; FcepsilonR; immunoglobulin E; IgE; atopic disease;
KW luminescence inducing protein; allergy; hyper IgE syndrome;
KW internal parasite infection; B cell neoplasia; ss.
XX
XX Homo sapiens.
XX
XX WO200104310-A1.
XX
XX 18-JAN-2001.
XX
XX 13-JUL-2000; 2000WO-US019070.
XX
XX 13-JUL-1999; 99US-0143612P.
XX
XX 02-MAR-2000; 2000US-0186412P.
XX
XX (HESK-) HESKA CORP.
XX
XX (PROM-) PROMEGA CORP.
XX
XX Weber ER, Wood KV, Hall MP;
XX
XX WPI; 2001-103082/11.
XX
XX P-PSDB; AAB31585.
XX
XX A fusion protein, comprising an Fc epsilon receptor domain and a
XX luminescence inducing protein domain that induces a LP substrate to emit
XX light when contacted with the LP domain, useful for detecting
XX immunoglobulin (Ig) E.
XX
XX Claim 17; Page 61-62; 105pp; English.
XX
XX The present sequence encodes a human Fc epsilon receptor (FcepsilonR)
XX alpha-chain mature protein, that binds to immunoglobulin (Ig) E. The
XX FcepsilonR domain is used to produce a fusion protein, which also
XX comprises a luminescence inducing protein domain that induces a substrate
XX to emit light when contacted with the luminescence inducing protein
XX domain. The fusion protein may be used to detect IgE. It may also be used
XX to identify a compound capable of inhibiting FcepsilonR protein activity.
XX IGE antibody production is indicative of diseases such as allergies,

```


CC atopic disease, hyper IGE syndrome, internal parasite infections and B
 CC cell neoplasia. Detection of IGE production in an animal following
 CC therapy is indicative of the efficacy of the treatment, for example when
 CC using treatments intended to disrupt IGE production

XX Sequence 696 BP; 208 A; 150 C; 159 G; 179 T; 0 U; 0 Other;

Query Match 100.0%; Score 516; DB 5; Length 696;
 Best Local Similarity 100.0%; Pred. No. 2.4e-148;
 Matches 516; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GTCCCTCAGAACCTTAAGTCTCTTGAACCTCCATGGAATAGAATATTTAAAGGAGAG 60
 Db 1 GTCCCTCAGAACCTTAAGTCTCTTGAACCTCCATGGAATAGAATATTTAAAGGAGAG 60

QY 61 AATGTGACTCTTACATGTAATGGGAACAATTTCTTGAAGTCAGTTCACCAATGGTTC 120
 Db 61 AATGTGACTCTTACATGTAATGGGAACAATTTCTTGAAGTCAGTTCACCAATGGTTC 120

QY 121 CACAATGCGACCTTTTCAGAGAGACAAATTCAGTTTGAATATTTGAATGCAAAATTT 180
 Db 121 CACAATGCGACCTTTTCAGAGAGACAAATTCAGTTTGAATATTTGAATGCAAAATTT 180

QY 181 GAAGACAGTGGAGATACAAATGTCAGCACCAACAAATTAATGAGAGTGAACCTGTGTAC 240
 Db 181 GAAGACAGTGGAGATACAAATGTCAGCACCAACAAATTAATGAGAGTGAACCTGTGTAC 240

QY 241 CTGGAAGTCTTCACTGACTGCTCTCTTCAAGCCCTCTCTGAGGTCGTGATGGAGGC 300
 Db 241 CTGGAAGTCTTCACTGACTGCTCTCTTCAAGCCCTCTCTGAGGTCGTGATGGAGGC 300

QY 301 CAGCCCTCTTCTCAGGTCGATGTTGGAGAACCTGGATGTGTACAAAGTGTATCTAT 360
 Db 301 CAGCCCTCTTCTCAGGTCGATGTTGGAGAACCTGGATGTGTACAAAGTGTATCTAT 360

QY 361 TATAAGGATGTTGAAGTCTTCACTGACTGTTGAGAACCAACATCTCCATTACAAAT 420
 Db 361 TATAAGGATGTTGAAGTCTTCACTGACTGTTGAGAACCAACATCTCCATTACAAAT 420

QY 421 GCCACAGTTGAAGACAGTGAACCTACTGTACGGGCAAAAGTGTGGCAGCTGGACTAT 480
 Db 421 GCCACAGTTGAAGACAGTGAACCTACTGTACGGGCAAAAGTGTGGCAGCTGGACTAT 480

QY 481 GAGTCTCAGCCCTCAACATTACTGTAAATAAAGCT 516
 Db 481 GAGTCTCAGCCCTCAACATTACTGTAAATAAAGCT 516

RESULT 11
 AAQ55969 standard; DNA; 713 BP.
 ID AAQ55969;
 XX AAQ55969;
 AC AAQ55969;
 XX 25-MAR-2003 (revised)
 DT 12-SEP-1994 (first entry)
 XX Human dihydrofolate reductase (DHFR) gene.
 XX Dihydrofolate reductase; DHFR; marker; transformation; ss.
 XX Homo sapiens.
 XX Key Location/Qualifiers
 XX CDS 120..713
 XX /*tag= a
 XX /product= "Dihydrofolate reductase."

XX WO9403599-A1.
 XX 17-FEB-1994.
 XX 03-AUG-1993; 93WO-JP001085.

XX 04-AUG-1992; 92JP-00229227.
 PR 10-AUG-1992; 92JP-00213002.
 PR 08-OCT-1992; 92JP-00270513.
 PR 08-OCT-1992; 92JP-00270514.
 PR 08-OCT-1992; 92JP-00270515.
 XX (GREG) GREEN CROSS CORP.
 PA Ra C, Naito K, Hirama M, Okumura K;
 PI P-PSDB; AAR45778.
 XX WPI; 1994-065687/08.
 DR P-PSDB; AAR45778.
 XX Antiallergic peptide derived from high-affinity immunoglobulin E receptor
 PT - binds to human immunoglobulin E to block allergic reactions at source.
 XX Disclosure; Page 24-25; 37pp; Japanese.
 XX The dihydrofolate reductase (DHFR) gene was used in the construction of a
 CC vector as a selectable marker. The resulting vector was used to transform
 CC DHFR-deficient CHO cells. (Updated on 25-MAR-2003 to correct PN field.)
 XX Sequence 713 BP; 202 A; 166 C; 163 G; 182 T; 0 U; 0 Other;

Query Match 100.0%; Score 516; DB 2; Length 713;
 Best Local Similarity 100.0%; Pred. No. 2.5e-148;
 Matches 516; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GTCCCTCAGAACCTTAAGTCTCTTGAACCTCCATGGAATAGAATATTTAAAGGAGAG 60
 Db 195 GTCCCTCAGAACCTTAAGTCTCTTGAACCTCCATGGAATAGAATATTTAAAGGAGAG 254

QY 61 AATGTGACTCTTACATGTAATGGGAACAATTTCTTGAAGTCAGTTCACCAAAATGGTTC 120
 Db 255 AATGTGACTCTTACATGTAATGGGAACAATTTCTTGAAGTCAGTTCACCAAAATGGTTC 314

QY 121 CACAATGCGACCTTTTCAGAGAGACAAATTCAGTTTGAATATTTGAATGCAAAATTT 180
 Db 315 CACAATGCGACCTTTTCAGAGAGACAAATTCAGTTTGAATATTTGAATGCAAAATTT 374

QY 181 GAAGACAGTGGAGATACAAATGTCAGCACCAACAAAGTAAATGAGAGTGAACCTGTGTAC 240
 Db 375 GAAGACAGTGGAGATACAAATGTCAGCACCAACAAAGTAAATGAGAGTGAACCTGTGTAC 434

QY 241 CTGGAAGTCTTCACTGACTGCTCTCTTCAAGCCCTCTCTGAGGTCGTGATGGAGGC 300
 Db 435 CTGGAAGTCTTCACTGACTGCTCTCTTCAAGCCCTCTCTGAGGTCGTGATGGAGGC 494

QY 301 CAGCCCTCTTCTCAGTGGCCATGGTTGGAGAACCTGGATGTGTACAGAGTGAATCTAT 360
 Db 495 CAGCCCTCTTCTCAGTGGCCATGGTTGGAGAACCTGGATGTGTACAGAGTGAATCTAT 554

QY 361 TATAAGGATGTTGAAGTCTTCAAGTACTGTTGAGAACCAACATCTCCATTACAAAT 420
 Db 555 TATAAGGATGTTGAAGTCTTCAAGTACTGTTGAGAACCAACATCTCCATTACAAAT 614

QY 421 GCCACAGTTGAAGACAGTGAACCTACTGTACGGGCAAAAGTGTGGCAGCTGGACTAT 480
 Db 615 GCCACAGTTGAAGACAGTGAACCTACTGTACGGGCAAAAGTGTGGCAGCTGGACTAT 674

QY 481 GAGTCTCAGCCCTCAACATTACTGTAAATAAAGCT 516
 Db 675 GAGTCTCAGCCCTCAACATTACTGTAAATAAAGCT 710

RESULT 12
 AAV20402 standard; DNA; 773 BP.
 ID AAV20402
 XX AAV20402;
 AC AAV20402;
 XX 20-JUL-1998 (first entry)

XX	Human IgE receptor Fc-epsilon-R1 alpha chain DNA.	
DE	Fc-epsilon-R1 alpha chain; IgE receptor; human serum albumin;	
XX	fusion protein; allergy; atopic dermatitis; asthma; urticaria; hay fever;	
KW	eczema; anaphylaxis; gene therapy; diagnosis; transgenic animal; ds.	
KW		
XX	Homo sapiens.	
OS		
XX	Key	Location/Qualifiers
FF	sig_peptide	1..75
FT		/*tag= a
FT	mat_peptide	76..773
FT		/*tag= b
XX	WO9804718-A1.	
XX		
PD	05-FEB-1998.	
XX		
XX	25-JUL-1997;	97WO-EF004066.
XX		
PR	26-JUL-1996;	96US-00690216.
XX		
PA	(NOVS) NOVARTIS AG.	
XX		
PI	Digan ME, Lake P, Gram H;	
XX		
XX	WPI; 1998-130705/12.	
DR	P-PSDB; AAW48094.	
DR		
XX	New fusion polypeptide for, e.g. diagnosing allergies - comprises	
PT	immunoglobulin E-binding domain fused to human serum albumin.	
PT		
XX	Disclosure; Page 56; 77pp; English.	
PS		
XX	This nucleotide sequence codes the dominant form of full-length native	
CC	human IgE receptor Fc-epsilon R1 alpha chain (see AAW48094). A claimed	
CC	fusion protein (FP) comprises an IgE binding domain fused to at least one	
CC	human serum albumin (HSA) component (see AAW48095), optionally via a	
CC	peptide linker, and is especially a dimeric FP (see AAW48096) comprising	
CC	HSA fused, at each of its N- and C-termini, to the extracellular domain	
CC	(i.e. mature protein) of Fc-epsilon R1 alpha chain. Also claimed are: FP;	
CC	nucleic acids encoding the FP; a vector; a process for preparing the FP;	
CC	a method of performing gene therapy in humans that comprises removing	
CC	somatic cells from a patient. Genetically modifying them in culture by	
CC	insertion of a polynucleotide that encodes the FP, and reintroducing the	
CC	modified cells into the patient so that the FP is expressed by the cells	
CC	of the patient; and use of the FP in an in vitro diagnostic assay to	
CC	determine the level of IgE or auto-antibodies to Fc epsilon R1 in a	
CC	sample. The products can be used in the prevention and/or treatment of	
CC	IgE-mediated allergic diseases and related disorders such as atopic	
CC	dermatitis, atopic asthma, chronic urticaria, hayfever and eczema.	
CC	Compared with using IgE binding domain alone, the FP has a longer serum	
CC	life, and thus greater activity, without a loss of ability to bind serum	
CC	IgE or circulating auto-antibodies	
XX		
SQ	Sequence 773 BP; 220 A; 173 C; 176 G; 204 T; 0 U; 0 Other;	
	Query Match 100.0%; Score 516; DB 2; Length 773;	
	Best Local Similarity 100.0%; Pred. No. 2,6e-148;	
	Matches 516; Conservative 0; Mismatches 0; Indels 0; Gaps 0;	
QY	1 GTCCTCAGAAACCTAAGGTCCTCCTTGAACCCCTCCATGGAATAGATATTAAAGGAGAG 60	
DB	76 GTCCTCAGAAACCTAAGGTCCTCCTTGAACCCCTCCATGGAATAGATATTAAAGGAGAG 135	
QY	61 AATGTGACTCTTACATGTAATGGGACAAATTTCTTTGAAGTCAGTCCACCAATGGTTC 120	
DB	136 AATGTGACTCTTACATGTAATGGGACAAATTTCTTTGAAGTCAGTCCACCAATGGTTC 195	
QY	121 CACATGCGAGCCTTTCAGAGAGACAAATTCAGATTTGGAATATTGCAATGCCAAATTT 180	
DB	196 CACATGCGAGCCTTTCAGAGAGACAAATTCAGATTTGGAATATTGCAATGCCAAATTT 255	

QY	181 GAAGACAGTGGAGAAATACAAATGTCAGACCAACCAAGTTTAATGAGAGTGAACCTGTGTAC 240	
DB	256 GAAGACAGTGGAGAAATACAAATGTCAGACCAACCAAGTTTAATGAGAGTGAACCTGTGTAC 315	
QY	241 CTGGAAGTCTTCAAGTGAAGTGGCTGCTCCTTCAAGGCTCTGCTCAGGTGGTGGAGGGC 300	
DB	316 CTGGAAGTCTTCAAGTGAAGTGGCTGCTCCTTCAAGGCTCTGCTCAGGTGGTGGAGGGC 375	
QY	301 CAGCCCTCTCTCAGTGGCTGCTCCTTCAAGGCTCTGCTCAGGTGGTGGAGGGTGAATCTAT 360	
DB	376 CAGCCCTCTCTCAGTGGCTGCTCCTTCAAGGCTCTGCTCAGGTGGTGGAGGGTGAATCTAT 435	
QY	361 TATAAGGATGGTGAAGCTCTCAAGTACTGGTATGAGAACCAACATCTCCATTACAAAT 420	
DB	436 TATAAGGATGGTGAAGCTCTCAAGTACTGGTATGAGAACCAACATCTCCATTACAAAT 495	
QY	421 GCCACAGTTGAAGACAGTGAAGCTCTCAAGTACTGGTATGAGAACCAAGTGGAGCTGGACTAT 480	
DB	496 GCCACAGTTGAAGACAGTGAAGCTCTCAAGTACTGGTATGAGAACCAAGTGGAGCTGGACTAT 555	
QY	481 GAGTCTGAGCCCTCAACATTACTGTAAATAAAGCT 516	
DB	556 GAGTCTGAGCCCTCAACATTACTGTAAATAAAGCT 591	
RESULT 13		
ABS52959	standard; cDNA; 773 BP.	
XX	ABS52959;	
XX	29-NOV-2002 (first entry)	
XX	Human cDNA encoding IgE receptor FcepsilonR1alpha.	
XX	Human; gene; IgE receptor; FcepsilonR1alpha; HSA; human serum albumin;	
KW	antiallergic; dermatological; antiinflammatory; antiasthmatic; ss;	
KW	IgE binding domain; systemic allergy; IgE-receptor-mediated disorder;	
KW	atopic dermatitis; atopic asthma; chronic urticaria.	
OS	Homo sapiens.	
XX	Key	Location/Qualifiers
CDS	1..768	/*tag= a
FT	/partial	/product= "FcepsilonR1alpha"
FT	/note= "No stop codon shown"	
FT	Signal_peptide	1..75
FT		/*tag= b
FT	Mat_peptide	76..768
FT		/*tag= c
FT		/label= Mature_FcepsilonR1alpha
XX	US6423512-B1.	
XX	23-JUL-2002.	
XX	21-JUL-1997;	97US-00897956.
XX	26-JUL-1996;	96US-0022689P.
XX	(NOVS) NOVARTIS AG.	
XX	Digan ME, Lake P, Gram H;	
XX	WPI; 2002-672940/72.	
XX	P-PSDB; ABG32801.	
XX	New fusion IgE-binding polypeptide, useful for the prevention and	
PT	treatment of systemic allergy and/or other IgE-receptor-mediated	
PT	disorders such as atopic dermatitis, atopic asthma and chronic urticaria.	

XX

PS The invention relates to a new fusion polypeptide or its pharmaceutically

XX

CC acceptable salt comprises at least one IgE-binding domain fused to at
 CC least one human serum albumin (HSA) component, where the IgE-binding
 CC domain is the sequence (a) defined residues Val26-Leu204 of the protein
 CC sequence appearing as ABG32801, or a truncation at the carboxy terminus
 CC by 1-12 amino acids. Also included are: (1) a fusion polypeptide defined
 CC by residues Val26-Leu978 of the protein appearing as ABG32803; (2) a
 CC polynucleotide sequence encoding the fusion protein; (3) a host cell
 CC transformed with the polynucleotide; (4) a method of preparing the fusion
 CC protein comprising transforming a host cell with a vector comprising a
 CC polynucleotide encoding the fusion polypeptide, expressing the fusion
 CC polypeptide in the cell, and recovering the fusion polypeptide from the
 CC host cell, optionally in the form of its salt; and (5) a vector for
 CC expressing a polynucleotide sequence encoding a fusion polypeptide of
 CC formula (I), (II), (III), (IV), or (V) or its salts (R₁-L-R₂ (I), R₂-
 CC L-R₁ (II), R₁-L-R₂ (III), R₂-L-R₁ (IV), R₁-L-R₂ (I), R₂-L-R₁ (II),
 CC (V), where R₁ = the polypeptide (a) or its truncation at the carboxy
 CC terminus by 1-12 amino acids and R₂ = a polypeptide selected from the
 CC sequence defined by residues Asp25-Leu609 of the human HSA sequence
 CC appearing as ABG32802, or its truncation at the carboxy terminus by 1-10
 CC amino acids and L = independently a chemical bond, where the vector is
 CC PXMT3-Pla-HAS-Rla). The compositions and methods of the present invention
 CC are useful for the prevention and treatment of systemic allergy and other
 CC IgE-receptor-mediated disorders such as atopic dermatitis, atopic asthma,
 CC and chronic urticaria. The IgE-binding polypeptide have a more prolonged
 CC effective serum life, more improved clinical utility in the treatment of
 CC allergy, as well as improved activity in a more efficient and cost-
 CC effective manner. The present sequence encodes the human IgE receptor
 CC Fcεpsilon1α chain used to make the fusion protein of the invention

XX

SQ Sequence 773 BP; 220 A; 172 C; 177 G; 204 T; 0 U; 0 Other;

Query Match

Best Local Similarity 100.0%; Score 516; DB 6; Length 773;

Matches 516; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY

1 GTCCCTCAGAACCTAAGGTCCTCTGACCTCCATGGAATAGAAATATTAAAGGAGAG 60

DB

76 GTCCCTCAGAACCTAAGGTCCTCTGACCTCCATGGAATAGAAATATTAAAGGAGAG 135

QY

61 AATGTGACTCTTACATGTAATGGGAACAATTTCTTTGAAGTCAGTTCCACCAATGTTTC 120

DB

136 AATGTGACTCTTACATGTAATGGGAACAATTTCTTTGAAGTCAGTTCCACCAATGTTTC 195

QY

121 CACAATGGCAGCCCTTTCAGAGAGACAAATTCAGTTTGAATTTGTAATGTCACCAATTT 180

DB

196 CACAATGGCAGCCCTTTCAGAGAGACAAATTCAGTTTGAATTTGTAATGTCACCAATTT 255

QY

181 GAGACAGTGGAGAAATACAAATTCAGACCAACAAATTAATGAGAGTGAATGTTGATC 240

DB

256 GAGACAGTGGAGAAATACAAATTCAGACCAACAAATTAATGAGAGTGAATGTTGATC 315

QY

241 CTGGAAGTCTTTCAGTGAATGCTGCTTTCAGGCTCTGCTGAGTGGTGAATGAGGGC 300

DB

316 CTGGAAGTCTTTCAGTGAATGCTGCTTTCAGGCTCTGCTGAGTGGTGAATGAGGGC 375

QY

301 CAGCCCTCTTCTCAGTGGTCCATGTTGGAGAACTGGGATGTGACAAAGTGTATCTAT 360

DB

376 CAGCCCTCTTCTCAGTGGTCCATGTTGGAGAACTGGGATGTGACAAAGTGTATCTAT 435

QY

361 TATAAGGATGGTGAAGTCTCTCAGTGAATGCTGATGAGAACCAACATCTCCATTACAAT 420

DB

436 TATAAGGATGGTGAAGTCTCTCAGTGAATGCTGATGAGAACCAACATCTCCATTACAAT 495

QY

421 GCCACAGTTGAGACAGTGAAGTCTCTCAGTGAATGCTGATGAGAACCAACATCTCCATTACAAT 480

DB

496 GCCACAGTTGAGACAGTGAAGTCTCTCAGTGAATGCTGATGAGAACCAACATCTCCATTACAAT 555

QY

481 GAGTCTGAGCCCTCAACATTAATCTGTAATAAAGCT 516

DB

556 GAGTCTGAGCCCTCAACATTACTCTAATAAAGCT 591

RESULT 14

AAF97964

ID AAF97964 standard; cDNA; 774 BP.

XX

AC AAF97964;

XX

DT 19-JUN-2001 (first entry)

XX

Human immunoglobulin E receptor I alpha subunit coding sequence.

XX

Human; polymorphism; immunoglobulin E receptor I alpha subunit; IGERA;
 single nucleotide polymorphism; SNP; allele specific oligonucleotide;
 immunoassay; detection; ss.

XX

OS Homo sapiens.

XX

WO200111010-A2.

XX

PD 15-FEB-2001.

XX

PF 02-AUG-2000; 2000WO-US021097.

XX

PR 09-AUG-1999; 99US-0147860P.

XX

(GENA-) GENAISSANCE PHARM INC.

XX

Chew A, Denton RR, Duda A, Kitem SE, Lanz EM, Nandabalan K;
 Stephens JC;

XX

WPI; 2001-202766/20.

DR

P-PSDB; AAB74667.

PT

New polynucleotide for gene therapy, comprises nucleotide polymorphisms

XX

in the immunoglobulin E receptor I alpha subunit gene.

XX

Claim 7; Fig 2; 99pp; English.

XX

The present invention describes an isolated polynucleotide (I) comprising
 a nucleotide sequence (S) which is a polymorphic variant of a reference
 sequence for the human immunoglobulin E receptor I alpha subunit (IGERA)
 gene or its fragment. The polymorphic variant comprises at least one
 polymorphism selected from guanine (G) at polymorphic site (PS) 1, PS9,
 PS10 or PS21, cytosine (C) at PS2, PS3, PS6, PS12, PS18 or PS20, adenine
 (A) at PS5, PS7, PS11, PS13, PS14, PS15, PS19, or PS22 and thymine (T) at
 PS4, PS8, PS16 or PS17, or (G) at a position corresponding to nucleotide
 251, (A) at a position corresponding to nucleotide 302 or 741, and (T) at
 a position corresponding to nucleotide 530. (I) can be used in gene
 therapy. (I) is useful for therapeutic purposes. A polypeptide (II)
 encoded by (I) is useful in drug screening assays and in assays to
 measure the binding affinity of one or more candidate drugs targeting
 (II). An antibody (III) to (II) is useful to immunoprecipitate (II) from
 solution and also reacts with (II) on Western or immunoblots of
 polyacrylamide gels on membrane supports or substrates. (III) is also
 useful in immunoassays to detect (II) in biological samples. AAF97965 to
 AAF98096 represent IGERA allele specific oligonucleotide probes; AAF97965 to
 AAF98096 represent IGERA gene polymorphism detection primers; and
 AAF98141 to AAF98180 represent IGERA gene PCR primers which are used in
 the exemplification of the present invention. The present sequence
 encodes the human IGERA protein used in the present invention

XX

SQ Sequence 774 BP; 221 A; 172 C; 177 G; 204 T; 0 U; 0 Other;

Query Match

Best Local Similarity 100.0%; Score 516; DB 4; Length 774;

Matches 516; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY

1 GTCCCTCAGAACCTAAGGTCCTCTGACCTCCATGGAATAGAAATATTAAAGGAGAG 60

DB

76 GTCCCTCAGAACCTAAGGTCCTCTGACCTCCATGGAATAGAAATATTAAAGGAGAG 135

QY 61 AATGTGACTCTTACATGTAATGGGAACAATTTCTTTGAAGTCAGTTCCACCAAAATGGTTC 120
 DB 136 AATGTGACTCTTACATGTAATGGGAACAATTTCTTTGAAGTCAGTTCCACCAAAATGGTTC 195
 QY 121 CACAATGGCAGCCTTTCAAGAGACACAAATTTCAAGTTTGAATTTGTAATGCAAAATTT 180
 DB 196 CACAATGGCAGCCTTTCAAGAGACACAAATTTCAAGTTTGAATTTGTAATGCAAAATTT 255
 QY 181 GAAGCAGTGGAGATCAAAATGTCAGACCAACCAAGTTAATGAGAGTGAACCTGTGTAC 240
 DB 256 GAAGCAGTGGAGATCAAAATGTCAGACCAACCAAGTTAATGAGAGTGAACCTGTGTAC 315
 QY 241 CTGGAAGTCTTCAAGTACTGCTCTCTTCAAGCCTCTCTGAGGTGGTGTGAGGGC 300
 DB 316 CTGGAAGTCTTCAAGTACTGCTCTCTTCAAGCCTCTCTGAGGTGGTGTGAGGGC 375
 QY 301 CAGCCCTCTTCTCAGTGCCATGGTTGGAGAACTGGGATGTAACAAGTGTACTAT 360
 DB 376 CAGCCCTCTTCTCAGTGCCATGGTTGGAGAACTGGGATGTAACAAGTGTACTAT 435
 QY 361 TATAAGGATGGTGAAGCTCTCAAGTACTGCTGATGAGAACCAACATCTCCATTACAAAT 420
 DB 436 TATAAGGATGGTGAAGCTCTCAAGTACTGCTGATGAGAACCAACATCTCCATTACAAAT 495
 QY 421 GCCACAGTTGAAGCAGTGGAACTTACTGTAAGCGGCAAGTGTGGCAGTGGACTAT 480
 DB 496 GCCACAGTTGAAGCAGTGGAACTTACTGTAAGCGGCAAGTGTGGCAGTGGACTAT 555
 QY 481 GAGTCTGAGCCCTCAACATTACTGTAATAAAAGCT 516
 DB 556 GAGTCTGAGCCCTCAACATTACTGTAATAAAAGCT 591

RESULT 15

AAQ27267
 ID AAQ27267 standard; DNA; 851 BP.
 XX AC AAQ27267;
 XX DT 25-MAR-2003 (revised)
 XX DT 02-FEB-1993 (first entry)
 XX DE Human FcERI alpha-subunit and IL-2 hybrid gene.
 XX KW High affinity Fc immunoglobulin E receptor; IgE; antibody; interleukin-2;
 XX KW histamine release; allergy; ss.
 XX OS Homo sapiens.
 XX FH Key
 XX FT CDS
 XX FT Location/Qualifiers
 XX FT 107..806
 XX FT /*tag= a
 XX FT /product= "alpha-subunit_IL-2"

EP499112-A1.

XX PD 19-AUG-1992.

XX PF 03-FEB-1992; 92EP-00101732.

XX PR 11-FEB-1991; 91US-00653936.

XX PA (HOFF) HOFFMANN LA ROCHE & CO AG F.

XX PI Chizzonite RA, Hakimi J, Kochan JP;

XX DR WPI; 1992-277871/34.

XX PT Monoclonal antibodies bind to alpha sub-unit of Fc IgE receptor - for
 PT treatment and prevention of IgE induced allergic diseases, also for
 PT measuring alpha sub-unit and IgE levels in biological fluids.

XX PS Disclosure; Page 6; 30pp; English.

XX

This is a preferred hybrid gene for use in generating the monoclonal antibodies of the invention. The gene contains nucleotide sequence 121-710 of the human FcERI alpha-subunit to which nucleotides 876-1016 of the IL-2 receptor (the cytoplasmic and transmembrane regions) have been fused. (The nucleotide sequence of the human alpha-subunit is published in Nucleic Acid Research, 16(8):3584 (1988); the nucleotide sequence of the human p55 IL-2 receptor is published in Nature, 311:631 (1984).)
 CC Cytoplasmic and transmembrane regions from receptors other IL-2 receptor can be used. (Updated on 25-MAR-2003 to correct PN field.)
 XX

Sequence 851 BP; 241 A; 197 C; 204 G; 209 T; 0 U; 0 Other;

Query Match 100.0%; Score 516; DB 2; Length 851;

Best Local Similarity 100.0%; Pred. No. 2.7e-148; Indels 0; Gaps 0;

Matches 516; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GTCCCTCAGAAACCTAAGGTCTCTTGAACCTCCATGGAATAGATAATTTAAAGGAGAG 60

DB 182 GTCCCTCAGAAACCTAAGGTCTCTTGAACCTCCATGGAATAGATAATTTAAAGGAGAG 241

QY 61 AATGTGACTCTTACATGTAATGGGAACAATTTCTTTGAAGTCAGTTCCACCAAAATGGTTC 120

DB 242 AATGTGACTCTTACATGTAATGGGAACAATTTCTTTGAAGTCAGTTCCACCAAAATGGTTC 301

QY 121 CACAATGGCAGCCTTTCAAGAGACACAAATTTCAAGTTTGAATTTGTAATGCAAAATTT 180

DB 302 CACAATGGCAGCCTTTCAAGAGACACAAATTTCAAGTTTGAATTTGTAATGCAAAATTT 361

QY 181 GAAGCAGTGGAGATCAAAATGTCAGACCAACCAAGTTAATGAGAGTGAACCTGTGTAC 240

DB 362 GAAGCAGTGGAGATCAAAATGTCAGACCAACCAAGTTAATGAGAGTGAACCTGTGTAC 421

QY 241 CTGGAAGTCTTCAAGTACTGCTCTCTTCAAGCCTCTCTGAGGTGGTGTGAGGGC 300

DB 422 CTGGAAGTCTTCAAGTACTGCTCTCTTCAAGCCTCTCTGAGGTGGTGTGAGGGC 481

QY 301 CAGCCCTCTTCTCAGTGCCATGGTTGGAGAACTGGGATGTAACAAGTGTACTAT 360

DB 482 CAGCCCTCTTCTCAGTGCCATGGTTGGAGAACTGGGATGTAACAAGTGTACTAT 541

QY 361 TATAAGGATGGTGAAGCTCTCAAGTACTGTAATGAGAACCAACATCTCCATTACAAAT 420

DB 542 TATAAGGATGGTGAAGCTCTCAAGTACTGTAATGAGAACCAACATCTCCATTACAAAT 601

QY 421 GCCACAGTTGAAGCAGTGGAACTTACTGTAAGCGGCAAGTGTGGCAGTGGACTAT 480

DB 602 GCCACAGTTGAAGCAGTGGAACTTACTGTAAGCGGCAAGTGTGGCAGTGGACTAT 661

QY 481 GAGTCTGAGCCCTCAACATTACTGTAATAAAAGCT 516

DB 662 GAGTCTGAGCCCTCAACATTACTGTAATAAAAGCT 697

Search completed: October 8, 2004, 23:17:40

Job time : 251.898 secs

This Page Blank (uspto)

Sequence 11, Appl
Sequence 11, Appl
Sequence 6, Appl
Sequence 8, Appl
Sequence 6, Appl
Sequence 8, Appl
Sequence 4, Appl
Sequence 5, Appl
Sequence 5, Appl
Sequence 1, Appl
Sequence 3, Appl
Sequence 1, Appl
Sequence 3, Appl
Sequence 14, Appl
Sequence 15, Appl
Sequence 15, Appl

Sequence 11, Appl
Sequence 11, Appl
Sequence 6, Appl
Sequence 8, Appl
Sequence 6, Appl
Sequence 8, Appl
Sequence 4, Appl
Sequence 5, Appl
Sequence 5, Appl
Sequence 1, Appl
Sequence 3, Appl
Sequence 1, Appl
Sequence 3, Appl
Sequence 14, Appl
Sequence 15, Appl
Sequence 15, Appl

ALIGNMENTS

RESULT 1
US-08-756-387B-12
; Sequence 12, Application US/08756387B
; Patent No. 5945294
; GENERAL INFORMATION:
; APPLICANT: Frank, Glenn R.
; APPLICANT: Porter, James P.
; APPLICANT: Rushlow, Keith E.
; APPLICANT: Wassom, Donald L.
; TITLE OF INVENTION: Method to Detect Ige
; NUMBER OF SEQUENCES: 13
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Carol Talkington Verser, Ph.D.
; STREET: 1825 Sharp Point Drive
; CITY: Fort Collins
; STATE: Colorado
; COUNTRY: USA
; ZIP: 80525
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: Windows 95
; SOFTWARE: WordPerfect for Windows, Version 7.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/756,387B
; FILING DATE: No. 5945294ember 26, 1996
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Verser, Carol Talkington
; REGISTRATION NUMBER: 37,459
; REFERENCE/DOCKET NUMBER: DI-1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 970/493-7272
; TELEFAX: 970/484-9505
; INFORMATION FOR SEQ ID NO: 12:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 516 nucleotides
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: CDNA
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 1..516
; US-08-756-387B-12

Query Match 100.0%; Score 516; DB 2; Length 516;
Best Local Similarity 100.0%; Pred. No. 6.5e-16;
Matches 516; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Result No.	Score	Query Match	Length	ID	Description
1	516	100.0	516	2	US-08-756-387B-12
2	516	100.0	516	4	US-09-285-873-12
3	516	100.0	516	4	US-09-944-277A-12
4	516	100.0	591	2	US-08-756-387B-10
5	516	100.0	591	4	US-09-285-873-10
6	516	100.0	591	4	US-09-944-277A-10
7	516	100.0	699	2	US-08-756-387B-7
8	516	100.0	699	4	US-09-285-873-7
9	516	100.0	699	4	US-09-944-277A-7
10	516	100.0	713	2	US-08-238-027-3
11	516	100.0	773	4	US-08-897-956A-6
12	516	100.0	774	2	US-08-756-387B-4
13	516	100.0	774	2	US-08-756-387B-5
14	516	100.0	774	4	US-09-285-873-4
15	516	100.0	774	4	US-09-285-873-5
16	516	100.0	774	4	US-09-944-277A-4
17	516	100.0	774	4	US-09-944-277A-5
18	516	100.0	1174	1	US-07-869-933-10
19	516	100.0	1174	3	US-09-103-663-10
20	516	100.0	1198	2	US-08-756-387B-1
21	516	100.0	1198	2	US-08-756-387B-3
22	516	100.0	1198	4	US-09-285-873-1
23	516	100.0	1198	4	US-09-285-873-3
24	516	100.0	1198	4	US-09-944-277A-1
25	516	100.0	1198	4	US-09-944-277A-3
26	516	100.0	2955	4	US-08-897-956A-4
27	514.4	99.7	591	3	US-08-788-954-1

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Total number of hits satisfying chosen parameters: 1365418

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Issued Patents NA:
1: /cgn2_6/prodata/2/ina/5A COMB.seq.*
2: /cgn2_6/prodata/2/ina/5B COMB.seq.*
3: /cgn2_6/prodata/2/ina/6A COMB.seq.*
4: /cgn2_6/prodata/2/ina/6B COMB.seq.*
5: /cgn2_6/prodata/2/ina/PTUS COMB.seq.*
6: /cgn2_6/prodata/2/ina/backfiles1.seq.*

Title: US-10-763-400-12
Perfect score: 516
Sequence: 1 gccctcgaaacctaaggt.....acattactgtataaaagct 516

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 682709 seqs, 277475446 residues

GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.

OM nucleic - nucleic search, using sw model

Run on: October 10, 2004, 11:14:29 ; Search time 45.6178 Seconds
(without alignments)
6277.259 Million cell updates/sec

RESULT 4
US-08-756-387B-10
; Sequence 10, Application US/08756387B
; Patent No. 5945294
; GENERAL INFORMATION:
; APPLICANT: Frank, Glenn R.
; APPLICANT: Porter, James P.
; APPLICANT: Rushlow, Keith E.
; APPLICANT: Wassom, Donald L.
; TITLE OF INVENTION: Method to Detect IgE
; NUMBER OF SEQUENCES: 13
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Carol Talkington Verser, Ph.D.
; ADDRESS: Heskia Corporation
; STREET: 1825 Sharp Point Drive
; CITY: Fort Collins
; STATE: Colorado
; COUNTRY: USA
; ZIP: 80525
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: Windows 95
; SOFTWARE: Wordperfect for Windows, Version 7.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/756,387B
; FILING DATE: No. 5945294ember 26, 1996
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Verser, Carol Talkington
; REGISTRATION NUMBER: 37,459
; REFERENCE/DOCKET NUMBER: DI-1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 970/493-7272
; TELEFAX: 970/484-9505
; INFORMATION FOR SEQ ID NO: 10:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 591 nucleotides
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 1..591
; US-08-756-387B-10

Query Match 100.0%; Score 516; DB 2; Length 591;
Best Local Similarity 100.0%; Pred. No. 7.1e-161;
Matches 516; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GTCCTCAGAAACCTTAAGTCTCTTGAACCCCTCCATGGAATAGATATTTAAAGGAGAG 60
Db 76 GTCCTCAGAAACCTTAAGTCTCTTGAACCCCTCCATGGAATAGATATTTAAAGGAGAG 135
Qy 61 AATGTGACTCTTACATGTAATGGGAACAAATTTCTTTGAAGTCAGTTCACCAAAATGGTTTC 120
Db 136 AATGTGACTCTTACATGTAATGGGAACAAATTTCTTTGAAGTCAGTTCACCAAAATGGTTTC 195
Qy 121 CACAATGGCAGCCTTTCCAGACAGACAAATTCAGTTTGAATATTGTGAATCCCAATTT 180
Db 196 CACAATGGCAGCCTTTCCAGACAGACAAATTCAGTTTGAATATTGTGAATCCCAATTT 255
Qy 181 GAAGACAGTGGAGATACAAATGTGAGCACCACCAAGTTAATGAGAGTGAACCTGTGTAC 240
Db 256 GAAGACAGTGGAGATACAAATGTGAGCACCACCAAGTTAATGAGAGTGAACCTGTGTAC 315
Qy 241 CTGGAAGTCTTTCAGTCACTGGTCTCTTCCTTCAGGCTCTGCTGAGGTGTGTGAGGGC 300
Db 316 CTGGAAGTCTTTCAGTCACTGGTCTCTTCCTTCAGGCTCTGCTGAGGTGTGTGAGGGC 375

COUNTRY: USA
ZIP: 80525
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: Windows 95
SOFTWARE: Wordperfect for Windows, Version 7.0
CURRENT APPLICATION DATA: US/09/944,277A
APPLICATION NUMBER: 09/285,873
FILING DATE: 1999-03-31
ATTORNEY/AGENT INFORMATION:
NAME: Verser, Carol Talkington
REGISTRATION NUMBER: 37,459
REFERENCE/DOCKET NUMBER: DI-1
TELECOMMUNICATION INFORMATION:
TELEPHONE: 970/493-7272
TELEFAX: 970/484-9505
INFORMATION FOR SEQ ID NO: 12:
SEQUENCE CHARACTERISTICS:
LENGTH: 516 nucleotides
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: cDNA
FEATURE:
NAME/KEY: CDS
LOCATION: 1..516
SEQUENCE DESCRIPTION: SEQ ID NO: 12:
US-09-944-277A-12

Query Match 100.0%; Score 516; DB 4; Length 516;
Best Local Similarity 100.0%; Pred. No. 6.5e-161;
Matches 516; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GTCCTCAGAAACCTTAAGTCTCTTGAACCCCTCCATGGAATAGATATTTAAAGGAGAG 60
Db 1 GTCCTCAGAAACCTTAAGTCTCTTGAACCCCTCCATGGAATAGATATTTAAAGGAGAG 60
Qy 61 AATGTGACTCTTACATGTAATGGGAACAAATTTCTTTGAAGTCAGTTCACCAAAATGGTTTC 120
Db 61 AATGTGACTCTTACATGTAATGGGAACAAATTTCTTTGAAGTCAGTTCACCAAAATGGTTTC 120
Qy 121 CACAATGGCAGCCTTTCCAGACAGACAAATTCAGTTTGAATATTGTGAATCCCAATTT 180
Db 121 CACAATGGCAGCCTTTCCAGACAGACAAATTCAGTTTGAATATTGTGAATCCCAATTT 180
Qy 181 GAAGACAGTGGAGATACAAATGTGAGCACCACCAAGTTAATGAGAGTGAACCTGTGTAC 240
Db 181 GAAGACAGTGGAGATACAAATGTGAGCACCACCAAGTTAATGAGAGTGAACCTGTGTAC 240
Qy 241 CTGGAAGTCTTTCAGTCACTGGTCTCTTCCTTCAGGCTCTGCTGAGGTGTGTGAGGGC 300
Db 241 CTGGAAGTCTTTCAGTCACTGGTCTCTTCCTTCAGGCTCTGCTGAGGTGTGTGAGGGC 300
Qy 301 CAGCCCTCTTCCTCAGTGGCCATGGTTGGAGGAACCTGGATGTGTACAAGGTGATCTAT 360
Db 301 CAGCCCTCTTCCTCAGTGGCCATGGTTGGAGGAACCTGGATGTGTACAAGGTGATCTAT 360
Qy 361 TATAAGGATGTGAGCTCTCAAGTACTGGTATGAGACCAACACATCTCCATTACAAAT 420
Db 361 TATAAGGATGTGAGCTCTCAAGTACTGGTATGAGACCAACACATCTCCATTACAAAT 420
Qy 421 GCCACAGTTGAAGCAGTGGAACTTACTTACTGTCAGGCAAGGTGTGGCAGCTGACTAT 480
Db 421 GCCACAGTTGAAGCAGTGGAACTTACTTACTGTCAGGCAAGGTGTGGCAGCTGACTAT 480
Qy 481 GAGTCTGAGCCCTCAACATTACTGTATAAAAGCT 516
Db 481 GAGTCTGAGCCCTCAACATTACTGTATAAAAGCT 516

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: Windows 95
SOFTWARE: WordPerfect for Windows, Version 7.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/756.387B
FILING DATE: No. 5945294ember 26, 1996
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Verser, Carol Talkington
REGISTRATION NUMBER: 37,459
REFERENCE/DOCKET NUMBER: DI-1
TELECOMMUNICATION INFORMATION:
TELEPHONE: 970/493-7272
TELEFAX: 970/484-9505
INFORMATION FOR SEQ ID NO: 7:
SEQUENCE CHARACTERISTICS:
LENGTH: 591 nucleotides
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: cDNA
FEATURE:
NAME/KEY: CDS
LOCATION: 1..591
US-08-756-387B-7

Query Match 100.0%; Score 516; DB 2; Length 591;
Best Local Similarity 100.0%; Pred. No. 7.9e-161;
Matches 516; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GTCCCTCAGAAACCTTAAGTCTCTTGAACCCCTCCATGGAATAGAATATTTAAAGGAGAG 60
DB 1 GTCCCTCAGAAACCTTAAGTCTCTTGAACCCCTCCATGGAATAGAATATTTAAAGGAGAG 60
QY 61 AATGTGACTCTTACATGTAATGGGAACAATTTCTTTGAAGTCAGTTCACCAATGGTTC 120
DB 61 AATGTGACTCTTACATGTAATGGGAACAATTTCTTTGAAGTCAGTTCACCAATGGTTC 120
QY 121 CACAATGGCAGCCTTTTCAAGAGAGACAATTTCAAGTTTGAATATTTGAATGCCAAATTT 180
DB 121 CACAATGGCAGCCTTTTCAAGAGAGACAATTTCAAGTTTGAATATTTGAATGCCAAATTT 180
QY 181 GAAGACAGTGGAGATACAAATGTGAGACCAACCAAGTTAATGAGAGTGAACCTGTGTAC 240
DB 181 GAAGACAGTGGAGATACAAATGTGAGACCAACCAAGTTAATGAGAGTGAACCTGTGTAC 240
QY 241 CTGGAAGTCTTCAAGTGAAGTGGTCTCTTCAAGCCCTCTGCTGAGGCTGTGATGGAGGC 300
DB 241 CTGGAAGTCTTCAAGTGAAGTGGTCTCTTCAAGCCCTCTGCTGAGGCTGTGATGGAGGC 300
QY 301 CAGCCCTCTTCTCAGTGGCCATGTTGGAGGAACCTGGATGTGTACAAAGTGTATCTAT 360
DB 301 CAGCCCTCTTCTCAGTGGCCATGTTGGAGGAACCTGGATGTGTACAAAGTGTATCTAT 360
QY 361 TATAAGGATGGTGAAGCTCTCAAGTACTGTGTATGAGAACCAACATCTCCATTACAAT 420
DB 361 TATAAGGATGGTGAAGCTCTCAAGTACTGTGTATGAGAACCAACATCTCCATTACAAT 420
QY 421 GCCACAGTTGAAGACAGTGGAACTTACTGTACGGCAAGTGTGCGAGCTGGACTAT 480
DB 421 GCCACAGTTGAAGACAGTGGAACTTACTGTACGGCAAGTGTGCGAGCTGGACTAT 480
QY 481 GAGTCTGAGCCCTCAACATTTACTGTATAAAGCT 516
DB 481 GAGTCTGAGCCCTCAACATTTACTGTATAAAGCT 516

RESULT 8
US-09-285-873-7
; Sequence 7, Application US/09285873
; Patent No. 6309832

INFORMATION FOR SEQ ID NO: 10:
SEQUENCE CHARACTERISTICS:
LENGTH: 591 nucleotides
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: cDNA
FEATURE:
NAME/KEY: CDS
LOCATION: 1..591
SEQUENCE DESCRIPTION: SEQ ID NO: 10:
US-09-944-277A-10

Query Match 100.0%; Score 516; DB 4; Length 591;
Best Local Similarity 100.0%; Pred. No. 7.1e-161;
Matches 516; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GTCCCTCAGAAACCTTAAGTCTCTTGAACCCCTCCATGGAATAGAATATTTAAAGGAGAG 60
DB 76 GTCCCTCAGAAACCTTAAGTCTCTTGAACCCCTCCATGGAATAGAATATTTAAAGGAGAG 135
QY 61 AATGTGACTCTTACATGTAATGGGAACAATTTCTTTGAAGTCAGTTCACCAATGGTTC 120
DB 136 AATGTGACTCTTACATGTAATGGGAACAATTTCTTTGAAGTCAGTTCACCAATGGTTC 195
QY 121 CACAATGGCAGCCTTTTCAAGAGAGACAATTTCAAGTTTGAATATTTGAATGCCAAATTT 180
DB 196 CACAATGGCAGCCTTTTCAAGAGAGACAATTTCAAGTTTGAATATTTGAATGCCAAATTT 255
QY 181 GAAGACAGTGGAGATACAAATGTGAGACCAACCAAGTTAATGAGAGTGAACCTGTGTAC 240
DB 256 GAAGACAGTGGAGATACAAATGTGAGACCAACCAAGTTAATGAGAGTGAACCTGTGTAC 315
QY 241 CTGGAAGTCTTCAAGTGAAGTGGTCTCTTCAAGCCCTCTGCTGAGGCTGTGATGGAGGC 300
DB 316 CTGGAAGTCTTCAAGTGAAGTGGTCTCTTCAAGCCCTCTGCTGAGGCTGTGATGGAGGC 375
QY 301 CAGCCCTCTTCTCAGTGGCCATGTTGGAGGAACCTGGATGTGTACAAAGTGTATCTAT 360
DB 376 CAGCCCTCTTCTCAGTGGCCATGTTGGAGGAACCTGGATGTGTACAAAGTGTATCTAT 435
QY 361 TATAAGGATGGTGAAGCTCTCAAGTACTGTGTATGAGAACCAACATCTCCATTACAAT 420
DB 436 TATAAGGATGGTGAAGCTCTCAAGTACTGTGTATGAGAACCAACATCTCCATTACAAT 495
QY 421 GCCACAGTTGAAGACAGTGGAACTTACTGTACGGGCAAGTGTGCGAGCTGGACTAT 480
DB 496 GCCACAGTTGAAGACAGTGGAACTTACTGTACGGGCAAGTGTGCGAGCTGGACTAT 555
QY 481 GAGTCTGAGCCCTCAACATTTACTGTATAAAGCT 516
DB 556 GAGTCTGAGCCCTCAACATTTACTGTATAAAGCT 591

RESULT 7
US-08-756-387B-7
; Sequence 7, Application US/08756387B
; Patent No. 5945294
; GENERAL INFORMATION:
; APPLICANT: Frank, Glenn R.
; APPLICANT: Porter, James P.
; APPLICANT: Rushlow, Keith E.
; APPLICANT: Wasson, Donald L.
; TITLE OF INVENTION: Method to Detect Ige
; NUMBER OF SEQUENCES: 13
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Carol Talkington Verser, Ph.D.
; ADDRESSEE: Heskia Corporation
; STREET: 1825 Sharp Point Drive
; CITY: Fort Collins
; STATE: Colorado
; COUNTRY: USA
; ZIP: 80525

```

; GENERAL INFORMATION:
; APPLICANT: Frank, Glenn R.
; APPLICANT: Porter, James P.
; APPLICANT: Rushlow, Keith E.
; APPLICANT: Wassom, Donald L.
; TITLE OF INVENTION: Method to Detect Ige
; NUMBER OF SEQUENCES: 13
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Carol Talkington Verser, Ph.D.
; ADDRESSEE: Heska Corporation
; STREET: 1825 Sharp Point Drive
; CITY: Fort Collins
; STATE: Colorado
; COUNTRY: USA
; ZIP: 80525
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: Windows 95
; SOFTWARE: WordPerfect for Windows, Version 7.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/285,873
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/08/756,387
; FILING DATE: No. 6309832ember 26, 1996
; ATTORNEY/AGENT INFORMATION:
; NAME: Verser, Carol Talkington
; REGISTRATION NUMBER: 37,459
; REFERENCE/DOCKET NUMBER: DI-1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 970/493-7272
; TELEFAX: 970/484-9505
; INFORMATION FOR SEQ ID NO: 7:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 699 nucleotides
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 1..699
; US-09-285-873-7

Query Match      100.0%; Score 516; DB 4; Length 699;
Best Local Similarity 100.0%; Pred. No. 7.9e-161; Indels 0; Gaps 0;
Matches 516; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GTCCTCAGAAACCTAAGGTCCTCTGAAACCTCCATGGAATAGAATATTTAAAGGAGAG 60
DB 1 GTCCTCAGAAACCTAAGGTCCTCTGAAACCTCCATGGAATAGAATATTTAAAGGAGAG 60

QY 61 AATGTGACTCTTACATGTAATGGGAACAATTTCTTTGAAGTCAGTCCACCAATGGTTC 120
DB 61 AATGTGACTCTTACATGTAATGGGAACAATTTCTTTGAAGTCAGTCCACCAATGGTTC 120

QY 121 CACAATGGCAGCCTTTTCAGAAAGAGACAAATTTCAAGTTTGAATATTTGTGAATGCCAAATTT 180
DB 121 CACAATGGCAGCCTTTTCAGAAAGAGACAAATTTCAAGTTTGAATATTTGTGAATGCCAAATTT 180

QY 181 GAAGACAGTGAGAAATCAAAATGTGACACACAAAGTTAATGAGAGTGAACCTGTGTAC 240
DB 181 GAAGACAGTGAGAAATCAAAATGTGACACACAAAGTTAATGAGAGTGAACCTGTGTAC 240

QY 241 CTGGAAGCTTTCAGTGACTGGTCTCTCTCAGGCTCTGCTCAGGCTCTGCTGAGGTGGTGGAGGC 300
DB 241 CTGGAAGCTTTCAGTGACTGGTCTCTCTCAGGCTCTGCTCAGGCTCTGCTGAGGTGGTGGAGGC 300

QY 301 CAGCCCTCTTCTCAGTGCCATGGTTGGAGGAACTGGGATGTGTACAGGTGATCTAT 360
DB 301 CAGCCCTCTTCTCAGTGCCATGGTTGGAGGAACTGGGATGTGTACAGGTGATCTAT 360

```

```

QY 361 TATAAGGATGGTGAAGCTCTCAAGTACTGGTATGAGAACCAACATCTCCATTACAAAT 420
DB 361 TATAAGGATGGTGAAGCTCTCAAGTACTGGTATGAGAACCAACATCTCCATTACAAAT 420

QY 421 GCCACAGTTTGAAGACAGTGGAACTTACTACTCTAGGGCAAAAGTGTGGCAGCTGACTAT 480
DB 421 GCCACAGTTTGAAGACAGTGGAACTTACTACTCTAGGGCAAAAGTGTGGCAGCTGACTAT 480

QY 481 GAGTCTGAGCCCTCAACATTAATCTGTATAATAAAGCT 516
DB 481 GAGTCTGAGCCCTCAACATTAATCTGTATAATAAAGCT 516

RESULT 9
US-09-944-277A-7
; Sequence 7, Application US/09944277A
; Patent No. 6682894
; GENERAL INFORMATION:
; APPLICANT: Frank, Glenn R.
; APPLICANT: Porter, James P.
; APPLICANT: Rushlow, Keith E.
; APPLICANT: Wassom, Donald L.
; TITLE OF INVENTION: Method to Detect Ige
; NUMBER OF SEQUENCES: 13
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Carol Talkington Verser, Ph.D.
; ADDRESSEE: Heska Corporation
; STREET: 1825 Sharp Point Drive
; CITY: Fort Collins
; STATE: Colorado
; COUNTRY: USA
; ZIP: 80525
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: Windows 95
; SOFTWARE: WordPerfect for Windows, Version 7.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/944,277A
; FILING DATE: 30-Aug-2001
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 09/285,873
; FILING DATE: 1999-03-31
; ATTORNEY/AGENT INFORMATION:
; NAME: Verser, Carol Talkington
; REGISTRATION NUMBER: 37,459
; REFERENCE/DOCKET NUMBER: DI-1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 970/493-7272
; TELEFAX: 970/484-9505
; INFORMATION FOR SEQ ID NO: 7:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 699 nucleotides
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 1..699
; SEQUENCE DESCRIPTION: SEQ ID NO: 7:
; US-09-944-277A-7

Query Match      100.0%; Score 516; DB 4; Length 699;
Best Local Similarity 100.0%; Pred. No. 7.9e-161; Indels 0; Gaps 0;
Matches 516; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GTCCTCAGAAACCTAAGGTCCTCTGAAACCTCCATGGAATAGAATATTTAAAGGAGAG 60
DB 1 GTCCTCAGAAACCTAAGGTCCTCTGAAACCTCCATGGAATAGAATATTTAAAGGAGAG 60

```


Db 555 TATAAGGATGGTGAAGCTCTCAAGTACTGGTATGAGAAACCAACATCTCCATTACAAAT 614
Qy 421 GCCACAGTGGAGACAGTGGAACTACTACTGTACGGGAAAGTGGGAGCTGGACTAT 480
Db 615 GCCACAGTGGAGACAGTGGAACTACTACTGTACGGGAAAGTGGGAGCTGGACTAT 674
Qy 481 GAGTCTGAGCCCTCAACATCTACTGTATAAAGCT 516
Db 675 GAGTCTGAGCCCTCAACATCTACTGTATAAAGCT 710

RESULT 11
US-08-897-956A-6
; Sequence 6, Application US/08897956A
; Patent No. 6423512
; GENERAL INFORMATION:
; APPLICANT: Mary Ellen Digan
; APPLICANT: Philip Lake
; APPLICANT: Hermann Gram
; TITLE OF INVENTION: Fusion Polypeptides
; FILE REFERENCE: 600-7244/CPA
; CURRENT APPLICATION NUMBER: US/08/897,956A
; CURRENT FILING DATE: 1997-07-21
; PRIOR APPLICATION NUMBER: 60/022,689
; PRIOR FILING DATE: 1996-07-26
; NUMBER OF SEQ ID NOS: 38
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 6
; LENGTH: 773
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Fusion Polynucleotide
US-08-897-956A-6

Query Match 100.0%; Score 516; DB 4; Length 773;
Best Local Similarity 100.0%; Pred. No. 8.4e-161; Indels 0; Gaps 0;
Matches 516; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GTCCTCAGAAACCTAAGTCTCTTGAACCCCTCCATGGAATAGAAATTTAAAGGAGAG 60
Db 76 GTCCTCAGAAACCTAAGTCTCTTGAACCCCTCCATGGAATAGAAATTTAAAGGAGAG 135
Qy 61 AATGTGACTCTTACATGTAATGGAACTTTCTTTGAAGTCAAGTCCACCAATGGTTC 120
Db 136 AATGTGACTCTTACATGTAATGGAACTTTCTTTGAAGTCAAGTCCACCAATGGTTC 195
Qy 121 CACAATGGCAGCCCTTTCAGAGAGACAAATTTCAAGTTTGAATTTGTAATGCCAAATTT 180
Db 196 CACAATGGCAGCCCTTTCAGAGAGACAAATTTCAAGTTTGAATTTGTAATGCCAAATTT 255
Qy 181 GAAGACAGTGGAGAAATCAAAATGTGAGGAACTGGATGTGTACAAAGTGTATCTAT 240
Db 256 GAAGACAGTGGAGAAATCAAAATGTGAGGAACTGGATGTGTACAAAGTGTATCTAT 315
Qy 241 CTGGAAGTCTTCAAGTCAAGTGGTCTCTTCAAGCCCTCTGCTGAGTGTGTATGGAGGC 300
Db 316 CTGGAAGTCTTCAAGTCAAGTGGTCTCTTCAAGCCCTCTGCTGAGTGTGTATGGAGGC 375
Qy 301 CAGCCCTCTTCTCAGGTGCAATGGTGGAGAACTGGATGTGTACAAAGTGTATCTAT 360
Db 376 CAGCCCTCTTCTCAGGTGCAATGGTGGAGAACTGGATGTGTACAAAGTGTATCTAT 435
Qy 361 TATAAGATGCTCAAGTCTCAAGTACTGTATGAAACCAACATCTCCATTACAAT 420
Db 436 TATAAGATGCTCAAGTCTCAAGTACTGTATGAAACCAACATCTCCATTACAAT 495
Qy 421 GCCACAGTGGAGACAGTGGAACTACTACTGTACGGGAAAGTGGGAGCTGGACTAT 480
Db 496 GCCACAGTGGAGACAGTGGAACTACTACTGTACGGGAAAGTGGGAGCTGGACTAT 555
Qy 481 GAGTCTGAGCCCTCAACATCTACTGTATAAAGCT 516

Db 556 GAGTCTGAGCCCTCAACATTACTGTATAAAGCT 591

RESULT 12
US-08-756-387B-4
; Sequence 4, Application US/08756387B
; Patent No. 5945294
; GENERAL INFORMATION:
; APPLICANT: Frank, Glenn R.
; APPLICANT: Porter, James P.
; APPLICANT: Rushlow, Keith E.
; APPLICANT: Wassom, Donald L.
; TITLE OF INVENTION: Method to Detect Ige
; NUMBER OF SEQUENCES: 13
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Carol Talkington Verser, Ph.D.
; ADDRESSEE: Heska Corporation
; STREET: 1825 Sharp Point Drive
; CITY: Fort Collins
; STATE: Colorado
; COUNTRY: USA
; ZIP: 80525
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: Windows 95
; SOFTWARE: WordPerfect for Windows, Version 7.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/756,387B
; FILING DATE: No. 5945294ember 26, 1996
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Verser, Carol Talkington
; REGISTRATION NUMBER: 37,459
; REFERENCE/DOCKET NUMBER: DI-1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 970/493-7272
; TELEFAX: 970/484-9505
; INFORMATION FOR SEQ ID NO: 4:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 774 nucleotides
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 1..774
US-08-756-387B-4

Query Match 100.0%; Score 516; DB 2; Length 774;
Best Local Similarity 100.0%; Pred. No. 8.4e-161; Indels 0; Gaps 0;
Matches 516; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GTCCTCAGAAACCTAAGTCTCTTGAACCCCTCCATGGAATAGAAATTTAAAGGAGAG 60
Db 76 GTCCTCAGAAACCTAAGTCTCTTGAACCCCTCCATGGAATAGAAATTTAAAGGAGAG 135
Qy 61 AATGTGACTCTTACATGTAATGGAACTTTCTTTGAAGTCAAGTCCACCAATGGTTC 120
Db 136 AATGTGACTCTTACATGTAATGGAACTTTCTTTGAAGTCAAGTCCACCAATGGTTC 195
Qy 121 CACAATGGCAGCCCTTTCAGAGAGACAAATTTCAAGTTTGAATTTGTAATGCCAAATTT 180
Db 196 CACAATGGCAGCCCTTTCAGAGAGACAAATTTCAAGTTTGAATTTGTAATGCCAAATTT 255
Qy 181 GAAGACAGTGGAGAAATCAAAATGTGAGGAACTGGATGTGTACAAAGTGTATCTAT 240
Db 256 GAAGACAGTGGAGAAATCAAAATGTGAGGAACTGGATGTGTACAAAGTGTATCTAT 315
Qy 241 CTGGAAGTCTTCAAGTCAAGTGGTCTCTTCAAGCCCTCTGCTGAGTGTGTATGGAGGC 300
Db 316 CTGGAAGTCTTCAAGTCAAGTGGTCTCTTCAAGCCCTCTGCTGAGTGTGTATGGAGGC 375

QY 301 CAGCCCTCTTCTCAGTGCCATGGTTGGAGGAACCTGGGATGTGTACAAAGTGATCTAT 360
Db 376 CAGCCCTCTTCTCAGTGCCATGGTTGGAGGAACCTGGGATGTGTACAAAGTGATCTAT 435
QY 361 TATAAGGATGGTGAAGCTCTCAAGTACTGGTATGAGAACCAACATCTCCATTACAAAT 420
Db 436 TATAAGGATGGTGAAGCTCTCAAGTACTGGTATGAGAACCAACATCTCCATTACAAAT 495
QY 421 GCCCAGTTGAAGACAGTGAAGCACTTACTGTACGGGCAAGGTGTGGCAGCTGGACTAT 480
Db 496 GCCCAGTTGAAGACAGTGAAGCACTTACTGTACGGGCAAGGTGTGGCAGCTGGACTAT 555
QY 481 GAGTCTGAGCCCTCAACATTACTGTATAAAGCT 516
Db 556 GAGTCTGAGCCCTCAACATTACTGTATAAAGCT 591
RESULT 13
US-08-756-387B-5/c
; Sequence 5, Application US/08756387B
; Patent No. 5945294
; GENERAL INFORMATION:
; APPLICANT: Frank, Glenn R.
; APPLICANT: Porter, James P.
; APPLICANT: Rushlow, Keith E.
; APPLICANT: Wassom, Donald L.
; TITLE OF INVENTION: Method to Detect Ige
; NUMBER OF SEQUENCES: 13
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Carol Talkington Verser, Ph.D.
; ADDRESSEE: Heska Corporation
; STREET: 1825 Sharp Point Drive
; CITY: Fort Collins
; STATE: Colorado
; COUNTRY: USA
; ZIP: 80525
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: Windows 95
; SOFTWARE: WordPerfect for Windows, Version 7.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/756,387B
; FILING DATE: No. 5945294ember 26, 1996
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Verser, Carol Talkington
; REGISTRATION NUMBER: 37,459
; REFERENCE/DOCKET NUMBER: DI-1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 970/493-7272
; TELEFAX: 970/484-9505
; INFORMATION FOR SEQ ID NO: 5:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 774 nucleotides
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: cdna
US-08-756-387B-5
Query Match 100.0%; Score 516; DB 2; Length 774;
Best Local Similarity 100.0%; Pred. No. 8.4e-161;
Matches 516; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 GTCCTCAGAAACCTAAGTCTCTTGAACCTCCATGGAATAGATATTTAAAGGAG 60
Db 699 GTCCTCAGAAACCTAAGTCTCTTGAACCTCCATGGAATAGATATTTAAAGGAG 640
QY 61 AATGTGACTCTACATGTAATGGGAACAATTTCTTTGAAGTCAGTTCACCAATGGTTC 120
Db 639 AATGTGACTCTTACATGTAATGGGAACAATTTCTTTGAAGTCAGTTCACCAATGGTTC 580

QY 121 CACAATGGCAGCCTTTCAGAGAGACAATTCAGTTTGAATATTGTGAATGCCAAATTT 180
Db 579 CACAATGGCAGCCTTTCAGAGAGACAATTCAGTTTGAATATTGTGAATGCCAAATTT 520
QY 181 GAAGACAGTGGGAGAAATACAAATGTGAGCACCACCAAGTTAATGAGAGTCAACCTGTGTAC 240
Db 519 GAAGACAGTGGGAGAAATACAAATGTGAGCACCACCAAGTTAATGAGAGTCAACCTGTGTAC 460
QY 241 CTGGAAGTCTTCAAGTGAAGTGGTCTCTTCAAGTGAAGTGGTCTCTCTGAGGTGGTGTGGAGGC 300
Db 459 CTGGAAGTCTTCAAGTGAAGTGGTCTCTTCAAGTGAAGTGGTCTCTCTGAGGTGGTGTGGAGGC 400
QY 301 CAGCCCTCTTCTCAGTGCCATGGTTGGAGGAACCTGGGATGTGTACAAAGTGATCTAT 360
Db 399 CAGCCCTCTTCTCAGTGCCATGGTTGGAGGAACCTGGGATGTGTACAAAGTGATCTAT 340
QY 361 TATAAGGATGGTGAAGCTCTCAAGTACTGGTATGAGAACCAACATCTCCATTACAAAT 420
Db 339 TATAAGGATGGTGAAGCTCTCAAGTACTGGTATGAGAACCAACATCTCCATTACAAAT 280
QY 421 GCCCAGTTGAAGACAGTGAAGCACTTACTGTACGGGCAAGGTGTGGCAGCTGGACTAT 480
Db 279 GCCCAGTTGAAGACAGTGAAGCACTTACTGTACGGGCAAGGTGTGGCAGCTGGACTAT 220
QY 481 GAGTCTGAGCCCTCAACATTACTGTATAAAGCT 516
Db 219 GAGTCTGAGCCCTCAACATTACTGTATAAAGCT 184
RESULT 14
US-09-285-873-4
; Sequence 4, Application US/09285873
; Patent No. 6309832
; GENERAL INFORMATION:
; APPLICANT: Frank, Glenn R.
; APPLICANT: Porter, James P.
; APPLICANT: Rushlow, Keith E.
; APPLICANT: Wassom, Donald L.
; TITLE OF INVENTION: Method to Detect Ige
; NUMBER OF SEQUENCES: 13
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Carol Talkington Verser, Ph.D.
; ADDRESSEE: Heska Corporation
; STREET: 1825 Sharp Point Drive
; CITY: Fort Collins
; STATE: Colorado
; COUNTRY: USA
; ZIP: 80525
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: Windows 95
; SOFTWARE: WordPerfect for Windows, Version 7.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/285,873
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/08/756,387
; FILING DATE: No. 6309832ember 26, 1996
; ATTORNEY/AGENT INFORMATION:
; NAME: Verser, Carol Talkington
; REGISTRATION NUMBER: 37,459
; REFERENCE/DOCKET NUMBER: DI-1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 970/493-7272
; TELEFAX: 970/484-9505
; INFORMATION FOR SEQ ID NO: 4:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 774 nucleotides
; TYPE: nucleic acid
; STRANDEDNESS: single

```

; TOPOLOGY: linear
; MOLECULE TYPE: CDNA
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 1..774
US-09-285-873-4

Query Match      100.0%; Score 516; DB 4; Length 774;
Best Local Similarity 100.0%; Pred. No. 8.4e-161;
Matches 516; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GTCCTCAGAACCTTAAGGCTCTCTGAACCCCTCCATGGAATAGATATTTAAAGGAGAG 60
DB 76 GTCCTCAGAACCTTAAGGCTCTCTGAACCCCTCCATGGAATAGATATTTAAAGGAGAG 135
QY 61 AATGTGACTCTTACATGTAATGGGAACAATTTCTTTGAAGTCAGTTCCACCAATGGTTC 120
DB 136 AATGTGACTCTTACATGTAATGGGAACAATTTCTTTGAAGTCAGTTCCACCAATGGTTC 195
QY 121 CACATGCGACCTTTTCAGAGAGACAAATTCAGTTTGAATTTGTAATGCCAAATTT 180
DB 196 CACATGCGACCTTTTCAGAGAGACAAATTCAGTTTGAATTTGTAATGCCAAATTT 255
QY 181 GAAGACAGTGGAGAATACAAATGTGACACCAACAAAGTTAATCAGAGTGAACCTGTGTAC 240
DB 256 GAAGACAGTGGAGAATACAAATGTGACACCAACAAAGTTAATCAGAGTGAACCTGTGTAC 315
QY 241 CTGGAAGTCTTCAGTGAAGTGGCTCTCTTCAGGCTCTGCTGAGGTGGTGTGAGGGGC 300
DB 316 CTGGAAGTCTTCAGTGAAGTGGCTCTCTTCAGGCTCTGCTGAGGTGGTGTGAGGGGC 375
QY 301 CAGCCCTCTCTTCAGTGGCTGCTCTTCAGGCTCTGCTGAGGTGGTGTGAGGGGC 360
DB 376 CAGCCCTCTCTTCAGTGGCTGCTCTTCAGGCTCTGCTGAGGTGGTGTGAGGGGC 435
QY 361 TATAAGGATGGTGAAGTCTCAAGTACTGATGATGAGAACCAACATCTCCATTACAAAT 420
DB 436 TATAAGGATGGTGAAGTCTCAAGTACTGATGATGAGAACCAACATCTCCATTACAAAT 495
QY 421 GCACAGTGAAGACAGTGAAGTCTCAAGTACTGATGATGAGAACCAACATCTCCATTACAAAT 480
DB 496 GCACAGTGAAGACAGTGAAGTCTCAAGTACTGATGATGAGAACCAACATCTCCATTACAAAT 555
QY 481 GAGTCTGAGCCCTCAACATTACTGTAATAAAGCT 516
DB 556 GAGTCTGAGCCCTCAACATTACTGTAATAAAGCT 591

```

RESULT 15

US-09-285-873-5/c
 ; Sequence 5, Application US/09285873
 ; Patent No. 6309832

GENERAL INFORMATION:

; APPLICANT: Frank, Glenn R.
 ; APPLICANT: Porter, James P.
 ; APPLICANT: Rushlow, Keith E.
 ; APPLICANT: Wassom, Donald L.
 ; TITLE OF INVENTION: Method to Detect IgE
 ; NUMBER OF SEQUENCES: 13
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: Carol Talkington Verser, Ph.D.
 ; ADDRESS: Heska Corporation
 ; STREET: 1825 Sharp Point Drive
 ; CITY: Fort Collins
 ; STATE: Colorado
 ; COUNTRY: USA
 ; ZIP: 80525
 ; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: Floppy disk
 ; COMPUTER: IBM PC compatible
 ; OPERATING SYSTEM: Windows 95
 ; SOFTWARE: WordPerfect for Windows, Version 7.0
 ; CURRENT APPLICATION DATA:

```

; APPLICATION NUMBER: US/09/285.873
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/08/756.387
; FILING DATE: No. 6309832ember 26, 1996
; ATTORNEY/AGENT INFORMATION:
; NAME: Verser, Carol Talkington
; REGISTRATION NUMBER: 37,459
; REFERENCE/DOCKET NUMBER: DI-1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 970/493-7272
; TELEFAX: 970/484-9505
; INFORMATION FOR SEQ ID NO: 5:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 774 nucleotides
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA
US-09-285-873-5

```

Query Match 100.0%; Score 516; DB 4; Length 774;
 Best Local Similarity 100.0%; Pred. No. 8.4e-161;
 Matches 516; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

QY 1 GTCCTCAGAACCTTAAGGCTCTCTGAACCCCTCCATGGAATAGATATTTAAAGGAGAG 60
DB 699 GTCCTCAGAACCTTAAGGCTCTCTGAACCCCTCCATGGAATAGATATTTAAAGGAGAG 640
QY 61 AATGTGACTCTTACATGTAATGGGAACAATTTCTTTGAAGTCAGTTCCACCAATGGTTC 120
DB 639 AATGTGACTCTTACATGTAATGGGAACAATTTCTTTGAAGTCAGTTCCACCAATGGTTC 580
QY 121 CACATGCGACCTTTTCAGAGAGACAAATTCAGTTTGAATTTGTAATGCCAAATTT 180
DB 579 CACATGCGACCTTTTCAGAGAGACAAATTCAGTTTGAATTTGTAATGCCAAATTT 520
QY 181 GAAGACAGTGGAGAATACAAATGTGACACCAACAAAGTTAATCAGAGTGAACCTGTGTAC 240
DB 519 GAAGACAGTGGAGAATACAAATGTGACACCAACAAAGTTAATCAGAGTGAACCTGTGTAC 460
QY 241 CTGGAAGTCTTCAGTGAAGTGGCTCTCTTCAGGCTCTGCTGAGGTGGTGTGAGGGGC 300
DB 459 CTGGAAGTCTTCAGTGAAGTGGCTCTCTTCAGGCTCTGCTGAGGTGGTGTGAGGGGC 400
QY 301 CAGCCCTCTCTTCAGTGGCTGCTCTTCAGGCTCTGCTGAGGTGGTGTGAGGGGC 360
DB 399 CAGCCCTCTCTTCAGTGGCTGCTCTTCAGGCTCTGCTGAGGTGGTGTGAGGGGC 340
QY 361 TATAAGGATGGTGAAGTCTCAAGTACTGATGATGAGAACCAACATCTCCATTACAAAT 420
DB 339 TATAAGGATGGTGAAGTCTCAAGTACTGATGATGAGAACCAACATCTCCATTACAAAT 280
QY 421 GCACAGTGAAGACAGTGAAGTCTCAAGTACTGATGATGAGAACCAACATCTCCATTACAAAT 480
DB 279 GCACAGTGAAGACAGTGAAGTCTCAAGTACTGATGATGAGAACCAACATCTCCATTACAAAT 220
QY 481 GAGTCTGAGCCCTCAACATTACTGTAATAAAGCT 516
DB 219 GAGTCTGAGCCCTCAACATTACTGTAATAAAGCT 184

```

Search completed: October 10, 2004, 11:20:19
 Job time : 45.6178 secs

Sequence 11, Appl
Sequence 6, Appl
Sequence 8, Appl
Sequence 4, Appl
Sequence 5, Appl
Sequence 1, Appl
Sequence 3, Appl
Sequence 29, Appl
Sequence 13731, A
Sequence 8, Appl
Sequence 1287, Ap
Sequence 124, Ap
Sequence 1254, Ap
Sequence 208, App
Sequence 140, App
Sequence 100, App
Sequence 994, App
Sequence 1268, Ap
Sequence 382, App
Sequence 382, App
Sequence 7, Appl
Sequence 2037, Ap
Sequence 266, App
Sequence 244, App
Sequence 22, Appl
Sequence 1906, Ap
Sequence 1906, Ap
Sequence 286, App
Sequence 13, Appl
Sequence 1, Appl

15 287.2 55.7 603 16 US-10-434-817-11
16 287.2 55.7 708 16 US-10-434-817-6
17 287.2 55.7 708 16 US-10-434-817-8
18 287.2 55.7 765 16 US-10-434-817-4
19 287.2 55.7 765 16 US-10-434-817-5
20 287.2 55.7 1015 16 US-10-434-817-1
21 287.2 55.7 1015 16 US-10-434-817-3
22 272 52.7 757 13 US-10-236-392-29
23 167.8 32.5 2202 15 US-10-198-846-13731
24 166.2 32.2 755 15 US-10-027-736A-8
25 166.2 32.2 887 17 US-10-641-643-1287
26 164.6 31.9 887 16 US-10-191-997-124
27 164.6 31.9 887 17 US-10-641-643-1254
28 164.6 31.9 887 17 US-10-717-597-208
29 164.6 31.9 887 17 US-10-775-169-140
30 164.6 31.9 2463 15 US-10-240-965-100
31 161.4 31.3 1977 13 US-09-873-367C-994
32 161.4 31.3 1977 13 US-10-240-425-1268
33 161.4 31.3 1977 13 US-10-342-887-382
34 161.4 31.3 1977 13 US-10-172-118-382
35 161.4 31.3 1977 17 US-10-775-169-35
36 158.2 30.7 765 15 US-10-027-736A-7
37 136.6 26.5 1318 12 US-10-152-319A-2037
38 136.6 26.5 1318 16 US-10-191-803-266
39 135 26.2 1341 16 US-10-388-934-244
40 132 25.6 1321 12 US-09-836-544-22
41 132 25.6 1321 13 US-10-342-887-1906
42 132 25.6 1321 13 US-10-172-118-1906
43 131.6 25.5 1398 9 US-09-925-301-286
44 130.4 25.3 1035 15 US-10-384-850-13
45 130.4 25.3 1074 15 US-10-027-736A-1

ALIGNMENTS

RESULT 1
US-03-944-277A-12
; Sequence 12, Application US/09944277A
; Patent No. US20020034771A1
; GENERAL INFORMATION:
; APPLICANT: Frank, Glenn R.
; Porter, James P.
; Rushlow, Keith E.
; Wasson, Donald L.
; TITLE OF INVENTION: Method to Detect Ige
; NUMBER OF SEQUENCES: 13
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Carol Talkington Verser, Ph.D.
; STREET: 1825 Sharp Point Drive
; CITY: Fort Collins
; STATE: Colorado
; COUNTRY: USA
; ZIP: 80525
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: Windows 95
; SOFTWARE: WordPerfect for Windows, Version 7.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/944,277A
; FILING DATE: 30-AUG-2001
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 09/285,873
; FILING DATE: 1999-03-31
; ATTORNEY/AGENT INFORMATION:
; NAME: Verser, Carol Talkington
; REGISTRATION NUMBER: 37,459
; REFERENCE/DOCKET NUMBER: DI-1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 970/493-7272

GenCore version 5.1.6
Copyright (c) 1993 - 2004 CompuGen Ltd.

OM nucleic - nucleic search, using sw model

Run on: October 10, 2004, 11:20:22 ; Search time 300.513 Seconds
(without alignments)
8701.874 Million cell updates/sec

Title: US-10-763-400-12
Perfect score: 516
Sequence: 1 gctccctcgaacacaaaggt.....acattactgtaataaaagct 516

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 3340653 seqs, 2534783454 residues
Total number of hits satisfying chosen parameters: 6681306

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Published Applications NA:
1: /cgn2_6/ptodata/1/pubpna/US07_PUBCOMB.seq:
2: /cgn2_6/ptodata/1/pubpna/PCT_NEW_PUB.seq:
3: /cgn2_6/ptodata/1/pubpna/US05_NEW_PUB.seq:
4: /cgn2_6/ptodata/1/pubpna/US06_PUBCOMB.seq:
5: /cgn2_6/ptodata/1/pubpna/US07_NEW_PUB.seq:
6: /cgn2_6/ptodata/1/pubpna/PCTUS_PUBCOMB.seq:
7: /cgn2_6/ptodata/1/pubpna/US08_NEW_PUB.seq:
8: /cgn2_6/ptodata/1/pubpna/US08_PUBCOMB.seq:
9: /cgn2_6/ptodata/1/pubpna/US09A_PUBCOMB.seq:
10: /cgn2_6/ptodata/1/pubpna/US09B_PUBCOMB.seq:
11: /cgn2_6/ptodata/1/pubpna/US09C_PUBCOMB.seq:
12: /cgn2_6/ptodata/1/pubpna/US09_NEW_PUB.seq:
13: /cgn2_6/ptodata/1/pubpna/US10A_PUBCOMB.seq:
14: /cgn2_6/ptodata/1/pubpna/US10B_PUBCOMB.seq:
15: /cgn2_6/ptodata/1/pubpna/US10C_PUBCOMB.seq:
16: /cgn2_6/ptodata/1/pubpna/US10D_PUBCOMB.seq:
17: /cgn2_6/ptodata/1/pubpna/US10_NEW_PUB.seq:
18: /cgn2_6/ptodata/1/pubpna/US60_NEW_PUB.seq:
19: /cgn2_6/ptodata/1/pubpna/US60_PUBCOMB.seq:

pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	516	100.0	516	9	US-09-944-277A-12
2	516	100.0	516	13	US-10-293-992-3
3	516	100.0	528	10	US-09-809-715-1
4	516	100.0	528	13	US-10-293-992-1
5	516	100.0	591	9	US-09-944-277A-10
6	516	100.0	699	9	US-09-944-277A-7
7	516	100.0	774	9	US-09-944-277A-4
8	516	100.0	774	9	US-09-944-277A-5
9	516	100.0	898	13	US-10-236-392-27
10	516	100.0	1198	9	US-09-944-277A-1
11	516	100.0	1198	9	US-09-944-277A-3
12	516	100.0	1198	9	US-09-962-832-244
13	516	100.0	1198	17	US-10-775-169-141
14	503.2	97.5	528	10	US-09-809-715-3


```
; TELEFAX: 970/484-9505
; INFORMATION FOR SEQ ID NO: 12:
; SEQUENCE CHARACTERISTICS:
;   LENGTH: 516 nucleotides
;   TYPE: nucleic acid
;   STRANDEDNESS: single
;   TOPOLOGY: linear
;   MOLECULE TYPE: cDNA
;   FEATURE:
;     NAME/KEY: CDS
;     LOCATION: 1..516
;   SEQUENCE DESCRIPTION: SEQ ID NO: 12:
US-09-944-277A-12

Query Match      100.0%; Score 516; DB 9; Length 516;
Best Local Similarity 100.0%; Pred. No. 2e-157;
Matches 516; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GTCCTCAGAAACCTAAGGTCCTCTTGAACCCCTCATGGAATAGAAATATTAAAGGAGAG 60
DB 1 GTCCTCAGAAACCTAAGGTCCTCTTGAACCCCTCATGGAATAGAAATATTAAAGGAGAG 60
QY 61 AATGTGACTCTTACATGTAATGGGAACAATTTCTTTGAAGTCAGTTCCACCAATGGTTC 120
DB 61 AATGTGACTCTTACATGTAATGGGAACAATTTCTTTGAAGTCAGTTCCACCAATGGTTC 120
QY 121 CACAATGGCAGCCTTTCAGAGAGACAAATTCAGTTTGAATTTGGAATGCCAAATTT 180
DB 121 CACAATGGCAGCCTTTCAGAGAGACAAATTCAGTTTGAATTTGGAATGCCAAATTT 180
QY 181 GAACACAGTCGAGATACAAATGTCAGCACCAACAAATTCAGTGAAGTCGACCTGTGTAC 240
DB 181 GAACACAGTCGAGATACAAATGTCAGCACCAACAAATTCAGTGAAGTCGACCTGTGTAC 240
QY 241 CTGGAAGTCCTTCAAGTACTGGCTCTCTTTCAGGCCCTCTCTCTGAGGTGGTGGAGGGC 300
DB 241 CTGGAAGTCCTTCAAGTACTGGCTCTCTTTCAGGCCCTCTCTCTGAGGTGGTGGAGGGC 300
QY 301 CAGCCCTCTTCTCAGTGCCTCATGTTGAGGAACCTGGATGTGTACAGGTGATCTAT 360
DB 301 CAGCCCTCTTCTCAGTGCCTCATGTTGAGGAACCTGGATGTGTACAGGTGATCTAT 360
QY 361 TATAAGATGTTGAAGTCTCAAGTACTGTGTATGAGAACCAACATCTCCATTACAAAT 420
DB 361 TATAAGATGTTGAAGTCTCAAGTACTGTGTATGAGAACCAACATCTCCATTACAAAT 420
QY 421 GCCACAGTTGAAGACAGTGGAACTTACTGTACGGGCAAGTGGCGAGCTGGACTAT 480
DB 421 GCCACAGTTGAAGACAGTGGAACTTACTGTACGGGCAAGTGGCGAGCTGGACTAT 480
QY 481 GAGTCTGAGCCCTCAACATTACTGTATATAAAGCT 516
DB 481 GAGTCTGAGCCCTCAACATTACTGTATATAAAGCT 516

RESULT 2
US-10-293-992-3
; Sequence 3, Application US/10293992
; Publication No. US20040033527A1
; GENERAL INFORMATION:
; APPLICANT: Jaretzky, Theodore S.
; APPLICANT: Garman, Scott Clayton
; APPLICANT: Kinet, Jean-Pierre
; TITLE OF INVENTION: METHODS OF USING A THREE-DIMENSIONAL MODEL OF A FC EPSILON RECEPTOR
; FILE REFERENCE: AL-3-Cl-1
; CURRENT APPLICATION NUMBER: US/10/293,992
; CURRENT FILING DATE: 2002-11-13
; PRIOR APPLICATION NUMBER: 09/434,193
; PRIOR FILING DATE: 1999-11-04
; PRIOR APPLICATION NUMBER: 60/107,219
; PRIOR FILING DATE: 1998-11-05
; NUMBER OF SEQ ID NOS: 6
```

```
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 3
; LENGTH: 516
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
;   NAME/KEY: CDS
;   LOCATION: (1)..(516)
;   OTHER INFORMATION:
;     US-10-293-992-3

Query Match      100.0%; Score 516; DB 13; Length 516;
Best Local Similarity 100.0%; Pred. No. 2e-157;
Matches 516; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GTCCTCAGAAACCTAAGGTCCTCTTGAACCCCTCATGGAATAGAAATATTAAAGGAGAG 60
DB 1 GTCCTCAGAAACCTAAGGTCCTCTTGAACCCCTCATGGAATAGAAATATTAAAGGAGAG 60
QY 61 AATGTGACTCTTACATGTAATGGGAACAATTTCTTTGAAGTCAGTTCCACCAATGGTTC 120
DB 61 AATGTGACTCTTACATGTAATGGGAACAATTTCTTTGAAGTCAGTTCCACCAATGGTTC 120
QY 121 CACAATGGCAGCCTTTCAGAGAGACAAATTCAGTTTGAATTTGGAATGCCAAATTT 180
DB 121 CACAATGGCAGCCTTTCAGAGAGACAAATTCAGTTTGAATTTGGAATGCCAAATTT 180
QY 181 GAACACAGTCGAGATACAAATGTCAGCACCAACAAATTCAGTGAAGTCGACCTGTGTAC 240
DB 181 GAACACAGTCGAGATACAAATGTCAGCACCAACAAATTCAGTGAAGTCGACCTGTGTAC 240
QY 241 CTGGAAGTCCTTCAAGTACTGGCTCTCTTTCAGGCCCTCTCTCTGAGGTGGTGGAGGGC 300
DB 241 CTGGAAGTCCTTCAAGTACTGGCTCTCTTTCAGGCCCTCTCTCTGAGGTGGTGGAGGGC 300
QY 301 CAGCCCTCTTCTCAGTGCCTCATGTTGAGGAACCTGGATGTGTACAGGTGATCTAT 360
DB 301 CAGCCCTCTTCTCAGTGCCTCATGTTGAGGAACCTGGATGTGTACAGGTGATCTAT 360
QY 361 TATAAGATGTTGAAGTCTCAAGTACTGTGTATGAGAACCAACATCTCCATTACAAAT 420
DB 361 TATAAGATGTTGAAGTCTCAAGTACTGTGTATGAGAACCAACATCTCCATTACAAAT 420
QY 421 GCCACAGTTGAAGACAGTGGAACTTACTGTACGGGCAAGTGGCGAGCTGGACTAT 480
DB 421 GCCACAGTTGAAGACAGTGGAACTTACTGTACGGGCAAGTGGCGAGCTGGACTAT 480
QY 481 GAGTCTGAGCCCTCAACATTACTGTATATAAAGCT 516
DB 481 GAGTCTGAGCCCTCAACATTACTGTATATAAAGCT 516

RESULT 3
US-09-809-715-1
; Sequence 1, Application US/09809715
; Publication No. US20030003502A1
; GENERAL INFORMATION:
; APPLICANT: Jaretzky, Theodore S.
; APPLICANT: Garman, Scott Clayton
; APPLICANT: Kinet, Jean-Pierre
; TITLE OF INVENTION: THREE-DIMENSIONAL MODEL OF A COMPLEX BETWEEN A FC EPSILON RECEPTOR AND AN ANTIBODY
; FILE REFERENCE: AL-8
; CURRENT APPLICATION NUMBER: US/09/809,715
; CURRENT FILING DATE: 2001-03-14
; PRIOR APPLICATION NUMBER: 60/189,853
; PRIOR FILING DATE: 2000-03-15
; NUMBER OF SEQ ID NOS: 6
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 1
; LENGTH: 528
```



```

;
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 09/285,873
; FILING DATE: 1999-03-31
; ATTORNEY/AGENT INFORMATION:
; NAME: Verser, Carol Talkington
; REGISTRATION NUMBER: 37,459
; REFERENCE/DOCKET NUMBER: DI-1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 970/493-7272
; TELEFAX: 970/484-9505
; INFORMATION FOR SEQ ID NO: 10:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 591 nucleotides
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 1..591
; SEQUENCE DESCRIPTION: SEQ ID NO: 10:
US-09-944-277A-10

Query Match 100.0%; Score 516; DB 9; Length 591;
Best Local Similarity 100.0%; Pred. No. 2.1e-157;
Matches 516; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GTCCCTCAGAACCTAAGGCTCTCTTGAACCTCCATGGGAATAGAAATATTAAAGGAGAG 60
DB 76 GTCCCTCAGAACCTAAGGCTCTCTTGAACCTCCATGGGAATAGAAATATTAAAGGAGAG 135
QY 61 AATGTGACTCTTACATGTAATGGGAACAATTTCTTGAAGTCAGTTCCACCAATGTTTC 120
DB 136 AATGTGACTCTTACATGTAATGGGAACAATTTCTTGAAGTCAGTTCCACCAATGTTTC 195
QY 121 CACAATGGCAGCCTTTTCAAGAGACAAATTCAGTTTGAATTTGAATTTGGAATGCCAAATTT 180
DB 196 CACAATGGCAGCCTTTTCAAGAGACAAATTCAGTTTGAATTTGAATTTGGAATGCCAAATTT 255
QY 181 GAACACAGTGGAGAAATACAAATGTCAGCACCAACAACTTAATGAGAGTGAACCTGTGTAC 240
DB 256 GAACACAGTGGAGAAATACAAATGTCAGCACCAACAACTTAATGAGAGTGAACCTGTGTAC 315
QY 241 CTGGAAGTCTTCAAGTACTGGCTCTCTTCAAGGCTCTCTTCAAGGCTCTCTTCAAGGCTCTAT 360
DB 316 CTGGAAGTCTTCAAGTACTGGCTCTCTTCAAGGCTCTCTTCAAGGCTCTCTTCAAGGCTCTAT 375
QY 301 CAGCCCTCTTCTCAGTGCCTGCTCTTCAAGGCTCTCTTCAAGGCTCTCTTCAAGGCTCTAT 420
DB 376 CAGCCCTCTTCTCAGTGCCTGCTCTTCAAGGCTCTCTTCAAGGCTCTCTTCAAGGCTCTAT 435
QY 361 TATAAGGATGGTGAAGCTCTCAAGTACTGGTATGAGAACCAACATCTCCATTACAAAT 420
DB 436 TATAAGGATGGTGAAGCTCTCAAGTACTGGTATGAGAACCAACATCTCCATTACAAAT 495
QY 421 GCCACAGTGAAGACAGTGAACCTACTACTGACGGGCAAGTGTGGCAGTGGACTAT 480
DB 496 GCCACAGTGAAGACAGTGAACCTACTACTGACGGGCAAGTGTGGCAGTGGACTAT 555
QY 481 GAGTCTGAGCCCTCAACATTACTGTAATAAAGCT 516
DB 556 GAGTCTGAGCCCTCAACATTACTGTAATAAAGCT 591

```

RESULT 6

```

US-09-944-277A-7
; Sequence 7, Application US/09944277A
; Patent No. US20020034771A1
; GENERAL INFORMATION:
; APPLICANT: Frank, Glenn R.
; Porter, James P.
; Rushlow, Keith E.
; Wassom, Donald L.

```

```

;
; TITLE OF INVENTION: Method to Detect Ige
; NUMBER OF SEQUENCES: 13
; CORRESPONDENCE ADDRESS:
; ADDRESSES: Carol Talkington Verser, Ph.D.
; STREET: 1825 Sharp Point Drive
; CITY: Fort Collins
; STATE: Colorado
; COUNTRY: USA
; ZIP: 80525
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk.
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: Windows 95
; SOFTWARE: WordPerfect for Windows, Version 7.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/944,277A
; FILING DATE: 30-Aug-2001
; CLASSIFICATION: <unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 09/285,873
; FILING DATE: 1999-03-31
; ATTORNEY/AGENT INFORMATION:
; NAME: Verser, Carol Talkington
; REGISTRATION NUMBER: 37,459
; REFERENCE/DOCKET NUMBER: DI-1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 970/493-7272
; TELEFAX: 970/484-9505
; INFORMATION FOR SEQ ID NO: 7:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 699 nucleotides
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 1..699
; SEQUENCE DESCRIPTION: SEQ ID NO: 7:
US-09-944-277A-7

```

```

Query Match 100.0%; Score 516; DB 9; Length 699;
Best Local Similarity 100.0%; Pred. No. 2.4e-157;
Matches 516; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GTCCCTCAGAACCTAAGGCTCTCTTGAACCTCCATGGGAATAGAAATATTAAAGGAGAG 60
DB 1 GTCCCTCAGAACCTAAGGCTCTCTTGAACCTCCATGGGAATAGAAATATTAAAGGAGAG 60
QY 61 AATGTGACTCTTACATGTAATGGGAACAATTTCTTGAAGTCAGTTCCACCAATGTTTC 120
DB 61 AATGTGACTCTTACATGTAATGGGAACAATTTCTTGAAGTCAGTTCCACCAATGTTTC 120
QY 121 CACAATGGCAGCCTTTTCAAGAGACAAATTCAGTTTGAATTTGAATTTGGAATGCCAAATTT 180
DB 121 CACAATGGCAGCCTTTTCAAGAGACAAATTCAGTTTGAATTTGAATTTGGAATGCCAAATTT 180
QY 181 GAACACAGTGGAGAAATACAAATGTCAGCACCAACAACTTAATGAGAGTGAACCTGTGTAC 240
DB 181 GAACACAGTGGAGAAATACAAATGTCAGCACCAACAACTTAATGAGAGTGAACCTGTGTAC 240
QY 241 CTGGAAGTCTTCAAGTACTGGCTCTCTTCAAGGCTCTCTTCAAGGCTCTCTTCAAGGCTCTAT 360
DB 241 CTGGAAGTCTTCAAGTACTGGCTCTCTTCAAGGCTCTCTTCAAGGCTCTCTTCAAGGCTCTAT 360
QY 301 CAGCCCTCTTCTCAGTGCCTGCTCTTCAAGGCTCTCTTCAAGGCTCTCTTCAAGGCTCTAT 360
DB 301 CAGCCCTCTTCTCAGTGCCTGCTCTTCAAGGCTCTCTTCAAGGCTCTCTTCAAGGCTCTAT 360
QY 361 TATAAGGATGGTGAAGCTCTCAAGTACTGGTATGAGAACCAACATCTCCATTACAAAT 420
DB 361 TATAAGGATGGTGAAGCTCTCAAGTACTGGTATGAGAACCAACATCTCCATTACAAAT 420

```

QY	421	GCACAGTTGAAGACAGCTGGAACTTACTGTACGGGGCAAAGTGTGGCAGCTGGACTAT	480
Db	421	GCACAGTTGAGACAGTGGAACTTACTGTACGGGGCAAAGTGTGGCAGCTGGACTAT	480
QY	481	GAGCTGAGCCCTCAACATTACTGTAATAAAAGCT	516
Db	481	GAGCTGAGCCCTCAACATTACTGTAATAAAAGCT	516

RESULT 7

US-09-944-277A-4
; Sequence 4, Application US/09944277A
; Patent No. US20020034771A1
; GENERAL INFORMATION:

Query Match	100.0%	Score 516;	DB 9;	Length 774;
Best Local Similarity	100.0%;	Pred. No. 2.5e-157;		
Matches 516;	Conservative 0;	Mismatches 0;	Indels 0;	Gaps 0;

QY	1	GTCCCTCGAAACCTTAGGTCCTTTGAACCCCTCCATGGAAATAGATAATTTTAAAGGACAG	60
Db	76	GTCCCTCGAAACCTTAGGTCCTTTGAACCCCTCCATGGAAATAGATAATTTTAAAGGACAG	135
QY	61	AATGTGACTCTTACATGTAATGGGAACAATTTCTTTTGAAGTCAGITCCACCAAAATGGTTC	120
Db	136	AATGTGACTCTTACATGTAATGGGAACAATTTCTTTGAGTCAGITCCACAAATATGGTTC	195

Qy	121	CACAAATGGCAGCCTTT	CAGAAGACACAAATTC	CAAGTTT	TGAAATATTT	GTGTAATGCCAAATTT	180
Db	196	CACAAATGGCAGCCTTT	CAGAAGACACAAATTC	CAAGTTT	TGAAATATTT	GTGTAATGCCAAATTT	255
Qy	181	GAAGACAGTGGAGAAAT	CAAAATGTCAGCACAA	CAAGTTT	AAATCAGAGTGAAC	CTGTGTAC	240
Db	256	GAAGACAGTGGAGAAAT	CAAAATGTCAGCACAA	CAAGTTT	AAATCAGAGTGAAC	CTGTGTAC	315
Qy	241	CTGGAAGTCTTT	CAGTGA	CTGCTCT	CTTTCAGG	CCCTCTGCTGAGTGTGTGATGGAGGC	300
Db	316	CTGGAAGTCTTT	CAGTGA	CTGCTCT	CTTTCAGG	CCCTCTGCTGAGTGTGTGATGGAGGC	375
Qy	301	CAGCCCCCTCTTC	CTCAGT	GCCATGGTT	TGGAGNA	CTGGGATGTGTACAAAGTGCATCTAT	360
Db	376	CAGCCCCCTCTTC	CTCAGT	GCCATGGTT	TGGAGNA	CTGGGATGTGTACAAAGTGCATCTAT	435
Qy	361	TATATAGGATGGTGAAGCT	CTCAAGT	ACTTGTTATGAGA	ACCACAAATCTCCATTTACAAT		420
Db	436	TATATAGGATGGTGAAGCT	CTCAAGT	ACTTGTTATGAGNA	CCCAACAATCTCCATTTACAAT		495
Qy	421	GCACAGATTTGAAGA	CAGTGG	AACTTACTTACTGTA	ACGGCAAAGTGTGGCAGCTGGACATAT		480
Db	496	GCACAGATTTGAAGA	CAGTGG	AACTTACTTACTGTA	ACGGCAAAGTGTGGCAGCTGGACATAT		555
Qy	481	GAGTCTGAGCCCTCA	ACATTTACTGT	TAAATAAAGCT		516	
Db	556	GAGTCTGAGCCCTCA	ACATTTACTGT	TAAATAAAGCT		591	

RESULT 8

US-09-944-277A-5/c
Sequence 5, Application US/09944277A
Patent No. US20020034771A1
GENERAL INFORMATION:
APPLICANT: Frank, Glenn R.
Porter, James P.
Rushlow, Keith E.
Wasson, Donald L.
TITLE OF INVENTION: Method to Detect IGE
NUMBER OF SEQUENCES: 13
CORRESPONDENCE ADDRESS:
ADDRESSEE: Carol Talkington Verser, Ph.D.
Heska Corporation
STREET: 1825 Sharp Point Drive
CITY: Fort Collins
STATE: Colorado
COUNTRY: USA
ZIP: 80525
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: Windows 95
SOFTWARE: WordPerfect for Windows, Version 7.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/944,277A
FILING DATE: 30-Aug-2001
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 09/285,873
FILING DATE: 1999-03-31
ATTORNEY/AGENT INFORMATION:
NAME: Verser, Carol Talkington
REGISTRATION NUMBER: 37,459
REFERENCE/DOCKET NUMBER: DI-1
TELECOMMUNICATION INFORMATION:
TELEPHONE: 970/493-7272
TELEFAX: 970/484-9505
INFORMATION FOR SEQ ID NO: 5:
SEQUENCE CHARACTERISTICS:
LENGTH: 774 nucleotides
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear

```
; MOLECULE TYPE: cDNA
; SEQUENCE DESCRIPTION: SEQ ID NO: 5:
US-09-944-277A-5

Query Match      100.0%; Score 516; DB 9; Length 774;
Best Local Similarity 100.0%; Pred. No. 2.5e-157;
Matches 516; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GTCCTCAGAACCTTAAGTCTCCTTGAACCTCCATGGAATAGAAATATTAAAGGAGAG 60
Db
699 GTCCCTCAGAACCTTAAGTCTCCTTGAACCTCCATGGAATAGAAATATTAAAGGAGAG 640
QY 61 AATGTGACTCTTACATGTAATGGGAAACAATTTCTTTGAAGTCAGTTCCACCAATGTTTC 120
Db
639 AATGTGACTCTTACATGTAATGGGAAACAATTTCTTTGAAGTCAGTTCCACCAATGTTTC 580
QY 121 CACATGCGAGCCCTTCAGAGAGACAAATTCAGTTTGAATTTGTAATGCAATGCCAATTT 180
Db
579 CACATGCGAGCCCTTCAGAGAGACAAATTCAGTTTGAATTTGTAATGCAATGCCAATTT 520
QY 181 GAAGACAGTGGAGAAATACAAATGTGAGCACCACCAACAAGTTAATGAGAGTGAACCTGTGTAC 240
Db
519 GAAGACAGTGGAGAAATACAAATGTGAGCACCACCAACAAGTTAATGAGAGTGAACCTGTGTAC 460
QY 241 CTGGAAGTCTTCAAGTCTGCTGCTCTTCAAGTCTGCTGCTGAGGCTCTGCTGAGGTGGTGGAGGC 300
Db
459 CTGGAAGTCTTCAAGTCTGCTGCTCTTCAAGTCTGCTGCTGAGGCTCTGCTGAGGTGGTGGAGGC 400
QY 301 CAGCCCTCTTCTCAGTGTGCTGCTGCTGAGGAGTGGATGTGTACAAGTGTATCTAT 360
Db
399 CAGCCCTCTTCTCAGTGTGCTGCTGCTGAGGAGTGGATGTGTACAAGTGTATCTAT 340
QY 361 TATAAGGATGTTGAAGTCTCAAGTCTGCTGCTGAGGAGTGGATGTGTACAAGTGTATCTAT 420
Db
339 TATAAGGATGTTGAAGTCTCAAGTCTGCTGCTGAGGAGTGGATGTGTACAAGTGTATCTAT 280
QY 421 GCCACAGTTGAAGACAGTGGAACTTACTGTGACGGGCAAGTGTGGAGCTGGACTAT 480
Db
279 GCCACAGTTGAAGACAGTGGAACTTACTGTGACGGGCAAGTGTGGAGCTGGACTAT 220
QY 481 GAGTCTGAGCCCTCAACATTACTGTATAAAGCT 516
Db
219 GAGTCTGAGCCCTCAACATTACTGTATAAAGCT 184

RESULT 9
US-10-236-392-27
; Sequence 27, Application US/10236392
; Publication No. US20040067490A1
; GENERAL INFORMATION:
; APPLICANT: Anderson, David W
; APPLICANT: Boldos, Ferenc L
; APPLICANT: Burgess, Catherine, E
; APPLICANT: Casman, Stacie J
; APPLICANT: Catterton, Elina
; APPLICANT: Chapoval, Andrei
; APPLICANT: Crabtree, Julie
; APPLICANT: Edinger, Shlomit, R
; APPLICANT: Ellerman, Karen
; APPLICANT: Gerlach, Valerie
; APPLICANT: Gorman, Linda
; APPLICANT: Grosse, William M
; APPLICANT: Gusev, Vladimir
; APPLICANT: Kekuda, Ramesh
; APPLICANT: LaRoche, William J
; APPLICANT: Li, Li
; APPLICANT: MacDougall, John R
; APPLICANT: Malyankar, Uriel M
; APPLICANT: Miller, Charles E
; APPLICANT: Millet, Isabelle
; APPLICANT: Padigaru, Muralidhara
; APPLICANT: Patturajan, Meera
; APPLICANT: Pena, Carol A
```

```
; APPLICANT: Peyman, John A
; APPLICANT: Pastelli, Luca
; APPLICANT: Reiger, Daniel K
; APPLICANT: Rothenberg, Mark E
; APPLICANT: Shencoy, Suresh
; APPLICANT: Shinkets, Richard A
; APPLICANT: Smithson, Glenda
; TITLE OF INVENTION: THERAPEUTIC POLYPEPTIDES, NUCLEIC ACIDS ENCODING SAME
; FILE REFERENCE: 21402-442A
; CURRENT APPLICATION NUMBER: US/10/236,392
; CURRENT FILING DATE: 2002-09-06
; PRIOR APPLICATION NUMBER: US09/540,763
; PRIOR FILING DATE: 2000-03-30
; PRIOR APPLICATION NUMBER: US60/390,155
; PRIOR FILING DATE: 2002-06-19
; PRIOR APPLICATION NUMBER: US09/635,949
; PRIOR FILING DATE: 2000-08-10
; PRIOR APPLICATION NUMBER: US60/318,765
; PRIOR FILING DATE: 2001-09-12
; PRIOR APPLICATION NUMBER: US60/357,303
; PRIOR FILING DATE: 2002-02-15
; PRIOR APPLICATION NUMBER: US60/367,753
; PRIOR FILING DATE: 2002-03-25
; PRIOR APPLICATION NUMBER: US60/369,479
; PRIOR FILING DATE: 2002-04-02
; PRIOR APPLICATION NUMBER: US09/659,634
; PRIOR FILING DATE: 2000-09-12
; PRIOR APPLICATION NUMBER: US60/318,120
; PRIOR FILING DATE: 2001-09-07
; PRIOR APPLICATION NUMBER: US60/318,130
; PRIOR FILING DATE: 2001-09-07
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 794
; SOFTWARE: Custom
; SEQ ID NO 27
; LENGTH: 898
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (26)...(797)
US-10-236-392-27

Query Match      100.0%; Score 516; DB 13; Length 898;
Best Local Similarity 100.0%; Pred. No. 2.5e-157;
Matches 516; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GTCCTCAGAACCTTAAGTCTCCTTGAACCTCCATGGAATAGAAATATTAAAGGAGAG 60
Db
101 GTCCCTCAGAACCTTAAGTCTCCTTGAACCTCCATGGAATAGAAATATTAAAGGAGAG 160
QY 61 AATGTGACTCTTACATGTAATGGGAAACAATTTCTTTGAAGTCAGTTCCACCAATGTTTC 120
Db
161 AATGTGACTCTTACATGTAATGGGAAACAATTTCTTTGAAGTCAGTTCCACCAATGTTTC 220
QY 121 CACATGCGAGCCCTTCAGAGAGACAAATTCAGTTTGAATTTGTAATGCAATGCCAATTT 180
Db
221 CACATGCGAGCCCTTCAGAGAGACAAATTCAGTTTGAATTTGTAATGCAATGCCAATTT 280
QY 181 GAAGACAGTGGAGAAATACAAATGTGAGCACCACCAACAAGTTAATGAGAGTGAACCTGTGTAC 240
Db
281 GAAGACAGTGGAGAAATACAAATGTGAGCACCACCAACAAGTTAATGAGAGTGAACCTGTGTAC 340
QY 241 CTGGAAGTCTTCAAGTCTGCTGCTCTTCAAGTCTGCTGCTGAGGCTCTGCTGAGGTGGTGGAGGC 300
Db
341 CTGGAAGTCTTCAAGTCTGCTGCTCTTCAAGTCTGCTGCTGAGGCTCTGCTGAGGTGGTGGAGGC 400
QY 301 CAGCCCTCTTCTCAGTGTGCTGCTGCTGAGGAGTGGATGTGTACAAGTGTATCTAT 360
Db
401 CAGCCCTCTTCTCAGTGTGCTGCTGCTGAGGAGTGGATGTGTACAAGTGTATCTAT 460
QY 361 TATAAGGATGTTGAAGTCTCAAGTCTGCTGCTGAGGAGTGGATGTGTACAAGTGTATCTAT 420
```

Db 461 TATAAGGATGGTGAAGCTCTCAAGTACTGGTATGAGAACCAACATCTCCATTACAAAT 520
QY 421 GCCACAGTTGAACAGACAGTGGAACTTACTGCTAGCGGCAAAAGTGTGGCAGCTGGACTAT 480
Db 521 GCCACAGTTGAACAGACAGTGGAACTTACTGCTAGCGGCAAAAGTGTGGCAGCTGGACTAT 580
QY 481 GAGTCTGAGCCCTCAACATTACTGTAATAAAGCT 516
Db 581 GAGTCTGAGCCCTCAACATTACTGTAATAAAGCT 616

RESULT 10
US-09-944-277A-1
; Sequence 1, Application US/09944277A
; Patent No. US20020034771A1
; GENERAL INFORMATION:
; APPLICANT: Frank, Glenn R.
; Porter, James P.
; Rushlow, Keith E.
; Wassom, Donald L.
; TITLE OF INVENTION: Method to Detect IGE
; NUMBER OF SEQUENCES: 13
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Carol Talkington Verser, Ph.D.
; STREET: 1825 Sharp Point Drive
; CITY: Fort Collins
; STATE: Colorado
; COUNTRY: USA
; ZIP: 80525
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: Windows 95
; SOFTWARE: WordPerfect for Windows, Version 7.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/944,277A
; FILING DATE: 30-Aug-2001
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 09/285,873
; FILING DATE: 1999-03-31
; ATTORNEY/AGENT INFORMATION:
; NAME: Verser, Carol Talkington
; REGISTRATION NUMBER: 37,459
; REFERENCE/DOCKET NUMBER: DI-1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 970/493-7272
; TELEFAX: 970/484-9505
; INFORMATION FOR SEQ ID NO: 1:
; NAME/KEY: CDS
; LOCATION: 107..877
; SEQUENCE DESCRIPTION: SEQ ID NO: 1:
US-09-944-277A-1

Query Match 100.0%; Score 516; DB 9; Length 1198;
Best Local Similarity 100.0%; Pred. No. 3.4e-157;
Matches 516; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GTCCCTCAGAACTTAAGTCTCTCGAACCTCCATGGAATAGAAATTTAAAGGAGAG 60
Db 182 GTCCCTCAGAACTTAAGTCTCTCGAACCTCCATGGAATAGAAATTTAAAGGAGAG 241
QY 61 AATGTGACTCTTACATGTAATGGGACAAATTTTGAAGTCAGTTCCACAAATGGTTC 120
Db 242 AATGTGACTCTTACATGTAATGGGACAAATTTTGAAGTCAGTTCCACAAATGGTTC 301

QY 121 CACAATGGCAGCCCTTTTCAGAAAGAGACAAATTTCAAGTTTGAATATTTGTAATGCCAAATTT 180
Db 302 CACAATGGCAGCCCTTTTCAGAAAGAGACAAATTTCAAGTTTGAATATTTGTAATGCCAAATTT 361
QY 181 GAACAGAGTGGAGAAATACAAATGTCAGACCAACAAAGTTAATGAGAGTGAACCTGTGTAC 240
Db 362 GAACAGAGTGGAGAAATACAAATGTCAGACCAACAAAGTTAATGAGAGTGAACCTGTGTAC 421
QY 241 CTGGAAGTCTTCAGTGAAGTGGCTCTCTTCAGGCGCTCTCTGAGGTTGGTGGAGGGC 300
Db 422 CTGGAAGTCTTCAGTGAAGTGGCTCTCTTCAGGCGCTCTCTGAGGTTGGTGGAGGGC 481
QY 301 CAGCCCTCTTCCTCAGGTGCCATGTTGGAGAACTGGGATGTGTACAAAGGTGATCTAT 360
Db 482 CAGCCCTCTTCCTCAGGTGCCATGTTGGAGAACTGGGATGTGTACAAAGGTGATCTAT 541
QY 361 TATAAGGATGGTGAAGCTCTCAAGTACTGTTATGAGAACCAACACATCTCCATTACAAAT 420
Db 542 TATAAGGATGGTGAAGCTCTCAAGTACTGTTATGAGAACCAACACATCTCCATTACAAAT 601
QY 421 GCCACAGTTGAAGACAGTGGAACTTACTGTAACGGGCAAAAGTGTGGCAGCTGGACTAT 480
Db 602 GCCACAGTTGAAGACAGTGGAACTTACTGTAACGGGCAAAAGTGTGGCAGCTGGACTAT 661
QY 481 GAGTCTGAGCCCTCAACATTACTGTAATAAAGCT 516
Db 662 GAGTCTGAGCCCTCAACATTACTGTAATAAAGCT 697

RESULT 11
US-09-944-277A-3/c
; Sequence 3, Application US/09944277A
; Patent No. US20020034771A1
; GENERAL INFORMATION:
; APPLICANT: Frank, Glenn R.
; Porter, James P.
; Rushlow, Keith E.
; Wassom, Donald L.
; TITLE OF INVENTION: Method to Detect IGE
; NUMBER OF SEQUENCES: 13
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Carol Talkington Verser, Ph.D.
; STREET: 1825 Sharp Point Drive
; CITY: Fort Collins
; STATE: Colorado
; COUNTRY: USA
; ZIP: 80525
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: Windows 95
; SOFTWARE: WordPerfect for Windows, Version 7.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/944,277A
; FILING DATE: 30-Aug-2001
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 09/285,873
; FILING DATE: 1999-03-31
; ATTORNEY/AGENT INFORMATION:
; NAME: Verser, Carol Talkington
; REGISTRATION NUMBER: 37,459
; REFERENCE/DOCKET NUMBER: DI-1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 970/493-7272
; TELEFAX: 970/484-9505
; INFORMATION FOR SEQ ID NO: 3:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1198 nucleotides
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 107..877
; SEQUENCE DESCRIPTION: SEQ ID NO: 1:
US-09-944-277A-1

Query Match 100.0%; Score 516; DB 9; Length 1198;
Best Local Similarity 100.0%; Pred. No. 3.4e-157;
Matches 516; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GTCCCTCAGAACTTAAGTCTCTCGAACCTCCATGGAATAGAAATTTAAAGGAGAG 60
Db 182 GTCCCTCAGAACTTAAGTCTCTCGAACCTCCATGGAATAGAAATTTAAAGGAGAG 241
QY 61 AATGTGACTCTTACATGTAATGGGACAAATTTTGAAGTCAGTTCCACAAATGGTTC 120
Db 242 AATGTGACTCTTACATGTAATGGGACAAATTTTGAAGTCAGTTCCACAAATGGTTC 301

```
;
;
; MOLECULE TYPE: cDNA
; SEQUENCE DESCRIPTION: SEQ ID NO: 3:
US-09-944-277A-3

Query Match
Best Local Similarity 100.0%; Score 516; DB 9; Length 1198;
Matches 516; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GTCCCTCAGAACCTTAAGGTCTCTTGAACCTCCATGGAATAGATAATTTAAAGGAGAG 60
DB 1017 GTCCCTCAGAACCTTAAGGTCTCTTGAACCTCCATGGAATAGATAATTTAAAGGAGAG 958
QY 61 AATGTGACTCTTACATGTAATGGGAACAATTTCTTTGAAGTCAGTTCACCAAAATGTTT 120
DB 957 AATGTGACTCTTACATGTAATGGGAACAATTTCTTTGAAGTCAGTTCACCAAAATGTTT 898
QY 121 CACAATGGCAGCCTTTTCAGAGAGACAAATTTCAAGTTTGAATATTTGTAATGCCAAATTT 180
DB 897 CACAATGGCAGCCTTTTCAGAGAGACAAATTTCAAGTTTGAATATTTGTAATGCCAAATTT 838
QY 181 GAAGACAGTGGAGAAATACAAATGTGAGCAACCAAGTTAATGAGAGTGAACCTGTGTAC 240
DB 837 GAAGACAGTGGAGAAATACAAATGTGAGCAACCAAGTTAATGAGAGTGAACCTGTGTAC 778
QY 241 CTGGAAGTCTTCAAGTGAAGTCTCTCAAGTCTCTGAGGCTCTGAGGCTGTGAGGAGGC 300
DB 777 CTGGAAGTCTTCAAGTGAAGTCTCTCAAGTCTCTGAGGCTCTGAGGCTGTGAGGAGGC 718
QY 301 CAGCCCTCTTCCAGTGGCCATGTTGGAGGAACCTGGGATGTGACAGGTGATCTAT 360
DB 717 CAGCCCTCTTCCAGTGGCCATGTTGGAGGAACCTGGGATGTGACAGGTGATCTAT 658
QY 361 TATAAGGATGGTGAAGTCTCAAGTCTCTGATGAGAACCAACACATCTCCATTACAAAT 420
DB 657 TATAAGGATGGTGAAGTCTCAAGTCTCTGATGAGAACCAACACATCTCCATTACAAAT 598
QY 421 GCCACAGTGAAGACAGTGGAACTTACTGTACGGGCAAGTGTGGCAGTGGACTAT 480
DB 597 GCCACAGTGAAGACAGTGGAACTTACTGTACGGGCAAGTGTGGCAGTGGACTAT 538
QY 481 CAGTCTGAGCCCTCAACATTACTGTATAAAAGCT 516
DB 537 CAGTCTGAGCCCTCAACATTACTGTATAAAAGCT 502

RESULT 12
US-09-962-832-244
; Sequence 244, Application US/09962832
; Patent No. US20020110821A1
; GENERAL INFORMATION:
; APPLICANT: Ebner, Reinhard
; TITLE OF INVENTION: Cancer Gene Determination and Therapeutic Screening Using Signatu
; FILE REFERENCE: 689290-74
; CURRENT APPLICATION NUMBER: US/09/962,832
; PRIOR FILING DATE: 2001-09-25
; PRIOR APPLICATION NUMBER: US/60/235,077
; PRIOR FILING DATE: 2000-09-25
; PRIOR APPLICATION NUMBER: US/60/235,280
; NUMBER OF SEQ ID NOS: 259
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 244
; LENGTH: 1198
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-962-832-244

Query Match
Best Local Similarity 100.0%; Score 516; DB 9; Length 1198;
Matches 516; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GTCCCTCAGAACCTTAAGGTCTCTTGAACCTCCATGGAATAGATAATTTAAAGGAGAG 60
DB 1017 GTCCCTCAGAACCTTAAGGTCTCTTGAACCTCCATGGAATAGATAATTTAAAGGAGAG 958
QY 61 AATGTGACTCTTACATGTAATGGGAACAATTTCTTTGAAGTCAGTTCACCAAAATGTTT 120
DB 957 AATGTGACTCTTACATGTAATGGGAACAATTTCTTTGAAGTCAGTTCACCAAAATGTTT 898
QY 121 CACAATGGCAGCCTTTTCAGAGAGACAAATTTCAAGTTTGAATATTTGTAATGCCAAATTT 180
DB 897 CACAATGGCAGCCTTTTCAGAGAGACAAATTTCAAGTTTGAATATTTGTAATGCCAAATTT 838
QY 181 GAAGACAGTGGAGAAATACAAATGTGAGCAACCAAGTTAATGAGAGTGAACCTGTGTAC 240
DB 837 GAAGACAGTGGAGAAATACAAATGTGAGCAACCAAGTTAATGAGAGTGAACCTGTGTAC 778
QY 241 CTGGAAGTCTTCAAGTGAAGTCTCTCAAGTCTCTGAGGCTCTGAGGCTGTGAGGAGGC 300
DB 777 CTGGAAGTCTTCAAGTGAAGTCTCTCAAGTCTCTGAGGCTCTGAGGCTGTGAGGAGGC 718
QY 301 CAGCCCTCTTCCAGTGGCCATGTTGGAGGAACCTGGGATGTGACAGGTGATCTAT 360
DB 717 CAGCCCTCTTCCAGTGGCCATGTTGGAGGAACCTGGGATGTGACAGGTGATCTAT 658
QY 361 TATAAGGATGGTGAAGTCTCAAGTCTCTGATGAGAACCAACACATCTCCATTACAAAT 420
DB 657 TATAAGGATGGTGAAGTCTCAAGTCTCTGATGAGAACCAACACATCTCCATTACAAAT 598
QY 421 GCCACAGTGAAGACAGTGGAACTTACTGTACGGGCAAGTGTGGCAGTGGACTAT 480
DB 597 GCCACAGTGAAGACAGTGGAACTTACTGTACGGGCAAGTGTGGCAGTGGACTAT 538
QY 481 CAGTCTGAGCCCTCAACATTACTGTATAAAAGCT 516
DB 537 CAGTCTGAGCCCTCAACATTACTGTATAAAAGCT 502

RESULT 13
US-10-775-169-141
; Sequence 141, Application US/10775169
; Publication No. US2004017543A1
; GENERAL INFORMATION:
; APPLICANT: Wyeth
; APPLICANT: Burczynski, Michael
; APPLICANT: Twine, Natalie
; APPLICANT: Dorner, Andrew
; APPLICANT: Trepicchio, William
; TITLE OF INVENTION: Method for Monitoring Drug Activities In Vivo
; FILE REFERENCE: AM101080 (031896-013000)
; CURRENT APPLICATION NUMBER: US/10/775,169
; CURRENT FILING DATE: 2004-02-11
; NUMBER OF SEQ ID NOS: 5278
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 141
; LENGTH: 1198
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-775-169-141

Query Match
Best Local Similarity 100.0%; Score 516; DB 17; Length 1198;
Matches 516; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GTCCCTCAGAACCTTAAGGTCTCTTGAACCTCCATGGAATAGATAATTTAAAGGAGAG 60
DB 182 GTCCCTCAGAACCTTAAGGTCTCTTGAACCTCCATGGAATAGATAATTTAAAGGAGAG 241
QY 61 AATGTGACTCTTACATGTAATGGGAACAATTTCTTTGAAGTCAGTTCACCAAAATGTTT 120
DB 242 AATGTGACTCTTACATGTAATGGGAACAATTTCTTTGAAGTCAGTTCACCAAAATGTTT 301
QY 121 CACAATGGCAGCCTTTTCAGAGAGACAAATTTCAAGTTTGAATATTTGTAATGCCAAATTT 180
```

Db 302 CACAAATGGCAGCCTTTTCAGAGAGACAAATTCAGTTTGAATTCGCAAAATTT 361
Qy 181 GAAGACAGTGGAGATACAAATTCAGACCAACCAAGTTAATGAGAGTGAACCTGTGTAC 240
Db 362 GAAGACAGTGGAGATACAAATTCAGACCAACCAAGTTAATGAGAGTGAACCTGTGTAC 421
Qy 241 CTGGAAGTCTTCAAGTGAAGTGGTCTCTTCCAGGCTCTGCTGAGTGGTGTGAGGGGC 300
Db 422 CTGGAAGTCTTCAAGTGAAGTGGTCTCTTCCAGGCTCTGCTGAGTGGTGTGAGGGGC 481
Qy 301 CAGCCCTCTTCTCAGGTCSCATGGTTGGAGAACTGGGATGTGTACAAAGTGTATCTAT 360
Db 482 CAGCCCTCTTCTCAGGTCSCATGGTTGGAGAACTGGGATGTGTACAAAGTGTATCTAT 541
Qy 361 TATAAGAGTGGTGAAGTCTTCAAGTGAAGTGTGTACAAACCAACATCTCCATTACAAAT 420
Db 542 TATAAGAGTGGTGAAGTCTTCAAGTGAAGTGTGTACAAACCAACATCTCCATTACAAAT 601
Qy 421 GCCACAGTTGAACAGACAGTGAAGTCTTCAAGTGAAGTGTGTACAAACCAACATCTCCATTACAAAT 480
Db 602 GCCACAGTTGAACAGACAGTGAAGTCTTCAAGTGAAGTGTGTACAAACCAACATCTCCATTACAAAT 661
Qy 481 GAGTCTGAGCCCTTCAACATTACTGTATAAAGCT 516
Db 662 GAGTCTGAGCCCTTCAACATTACTGTATAAAGCT 697

RESULT 14

US-09-809-715-3
; Sequence 3, Application US/09809715
; Publication No. US2003003502A1
; GENERAL INFORMATION:
; APPLICANT: Jaretzky, Theodore S.
; APPLICANT: Garman, Scott Clayton
; APPLICANT: Wurzburg, Beth A.
; APPLICANT: Kinet, Jean-Pierre
; TITLE OF INVENTION: THREE-DIMENSIONAL MODEL OF A COMPLEX BETWEEN A Fc
; TITLE OF INVENTION: EPSILON RECEPTOR ALPHA CHAIN AND A Fc REGION OF AN Ige
; TITLE OF INVENTION: ANTIBODY AND USES THEREOF
; FILE REFERENCE: AU-8
; CURRENT APPLICATION NUMBER: US/09/809,715
; CURRENT FILING DATE: 2001-03-14
; PRIOR APPLICATION NUMBER: 60/189,853
; PRIOR FILING DATE: 2000-03-15
; NUMBER OF SEQ ID NOS: 6
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 3
; LENGTH: 528
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (1)...(528)
US-09-809-715-3

Query Match 97.5%; Score 503.2; DB 10; Length 528;
Best Local Similarity 98.4%; Pred. No. 3e-153;
Matches 508; Conservative 0; Mismatches 8; Indels 0; Gaps 0;
Qy 1 GTCCTCAGAAACCTAAGTCTCTTGAACCCCTCCATGGAATAGATATTTAAAGGAG 60
Db 1 GTCCTCAGAAACCTAAGTCTCTTGAACCCCTCCATGGAATAGATATTTAAAGGAG 60
Qy 61 AATGTGACTCTTACATGTAATGGGAACAATTTCTTTGAAATGAGTCCACCAATGGTTC 120
Db 61 AATGTGACTCTTACATGTAATGGGAACAATTTCTTTGAAATGAGTCCACCAATGGTTC 120
Qy 121 CACAATGGCAGCCTTTGAGAGAGACAAATTCAGATTTGAATTTGAATGCCAAATTT 180
Db 121 CACAATGGCAGCCTTTGAGAGAGACAAATTCAGATTTGAATTTGAATGCCAAATTT 180
Qy 181 GAGCAGAGTGGAGATCAATGTGACCAACCAACCAAGTTAATGAGAGTGAACCTGTGTAC 240

Db 181 GAAGACAGTGGAGATACAAATTCAGACCAACCAAGTTGCTGAGAGTGAACCTGTGTAC 240
Qy 241 CTGGAAGTCTTCAAGTGAAGTGGTCTCTTCCAGGCTCTGCTGAGTGGTGTGAGGGGC 300
Db 241 CTGGAAGTCTTCAAGTGAAGTGGTCTCTTCCAGGCTCTGCTGAGTGGTGTGAGGGGC 300
Qy 301 CAGCCCTCTTCTCAGTGCATGGTTGGAGAACTGGGATGTGTACAAAGTGTATCTAT 360
Db 301 CAGCCCTCTTCTCAGTGCATGGTTGGAGAACTGGGATGTGTACAAAGTGTATCTAT 360
Qy 361 TATAAGAGTGGTGAAGTCTTCAAGTGAAGTGTGTACAAACCAACATCTCCATTACAAAT 420
Db 361 TATAAGAGTGGTGAAGTCTTCAAGTGAAGTGTGTACAAACCAACATCTCCATTACAAAT 420
Qy 421 GCCACAGTTGAACAGACAGTGAAGTCTTCAAGTGAAGTGTGTACAAACCAACATCTCCATTACAAAT 480
Db 421 GCCACAGTTGAACAGACAGTGAAGTCTTCAAGTGAAGTGTGTACAAACCAACATCTCCATTACAAAT 480
Qy 481 GAGTCTGAGCCCTTCAACATTACTGTATAAAGCT 516
Db 481 GAGTCTGAGCCCTTCAACATTACTGTATAAAGCT 516

RESULT 15

US-10-434-817-11
; Sequence 11, Application US/10434817
; Publication No. US20030235579A1
; GENERAL INFORMATION:
; APPLICANT: Weber, Eric R.
; APPLICANT: McCall, Catherine A.
; TITLE OF INVENTION: NOVEL EQUINE Fc EPSILON RECEPTOR ALPHA
; TITLE OF INVENTION: CHAIN NUCLEIC ACID MOLECULES, PROTEINS AND USES THEREOF
; NUMBER OF SEQUENCES: 12
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Heska Corporation
; STREET: 1825 Sharp Point Drive
; CITY: Fort Collins
; STATE: Colorado
; COUNTRY: USA
; ZIP: 80525
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: WordPerfect for Windows, Version 7.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/10/434,817
; FILING DATE: 08-May-2003
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/09/015,734
; FILING DATE: 29-JAN-1998
; ATTORNEY/AGENT INFORMATION:
; NAME: Verser, Carol Talkington
; REGISTRATION NUMBER: 37,459
; REFERENCE/DOCKET NUMBER: DI-4
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 970/493-7272
; TELEFAX: 970/484-9505
; INFORMATION FOR SEQ ID NO: 11:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 603 nucleotides
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 1...603
; SEQUENCE DESCRIPTION: SEQ ID NO: 11:
US-10-434-817-11

Query Match

55.7%; Score 287.2; DB 16; Length 603;

Best Local Similarity 77.2%; Pred. No. 1.1e-82;
Matches 349; Conservative 0; Mismatches 103; Indels 0; Gaps 0;

Qy	7	CAGAAACCTTAAGGTCTCTTGAACCCCTCCATGGAATAGAATATTTAAAGGAGAGAATGTG	66
Db	82	CGAAATCTACAGTCTCTTGAATCCCATGGAATAGAATATTTGAGGAGAGAATGTG	141
Qy	67	ACTCTTACATGTAATGGGAACAATTTCTTTGAAGTCAGTTCACCAAAATGGTTCACAAT	126
Db	142	ACTCTTACATGTAATAAGACAAGCCCTTAAAGGCAACTCCACTGAGTGACCTACAAC	201
Qy	127	GCACCCCTTCAGAGAGACAATTCAGTTTGAATTTGATGCAATGCCAAATTTGAAGAC	186
Db	202	AACCCACTTTAGAAGTGACAACACTTCAAGTTGAACATCACTAATGCCCTCACCCGAGC	261
Qy	187	AGTGAGAAATACAAATGTGACCAACCAAGTTAATGAGAGTGAACCTGTGTACTGGAA	246
Db	262	AGTGGGAATACAGATGTCGGAACAATGACTTGAACCTGAGTGAAGCTGTGCACCTAGAA	321
Qy	247	GTCTTCAGTGAAGTCTGCTCTTCAAGCCCTCTGCTGAGGTGGTGAAGGGGCCAGCC	306
Db	322	GTCTTCAGTGAAGTCTGCTCTTCAAGCCCTCTGCTGAGGTGGTGAAGGGGCCAGCC	381
Qy	307	CTCTTCTCAGTGGCCATGGTTGGAGGAACCTGGGATGTGTACAAAGGTGATCTATTATAAG	366
Db	382	CTCGTTCTCAGGTGCGGTGGTGGAGGATTGGGACGTCTTCAAGGTGAICTACTACAAG	441
Qy	367	GATGTGAAGCTCTCAAGTACTGGTATGAGAACCAACATCTCCATTACAATGCCACA	426
Db	442	GATGGCAAAACCCCTCGAGTACTGGTATGAGAACCAACATCTCCATTGAAAGTGCCACA	501
Qy	427	GTGGAAGACAGTGGACCTACTGTACGGG	458
Db	502	ACAGAAAACAGTGGCACCTATTACTGGAGGG	533

Search completed: October 11, 2004, 01:41:42
Job time : 301.613 secs

GenCore version 5.1.6
Copyright (c) 1993 - 2004 CompuGen Ltd.

OM nucleic - nucleic search, using sw model

Run on: October 10, 2004, 11:14:29 ; Search time 1741.12 Seconds
(without alignments)
8849.962 Million cell updates/sec

Title: US-10-763-400-12

Perfect score: 516
Sequence: 1 gccctcagaacctaaagt.....acattactgtataaaagct 516

Scoring table: IDENTITY NUC

Gapop 10.0 , Gapext 1.0

Searched: 27513289 seqs, 14931090276 residues

Total number of hits satisfying chosen parameters: 55026578

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :

```
EST:*
1: em_estba:*
2: em_estum:*
3: em_estin:*
4: em_estmu:*
5: em_estov:*
6: em_estpl:*
7: em_estro:*
8: em_hic:*
9: gb_esti:*
10: gb_est2:*
11: gb_hic:*
12: gb_est3:*
13: gb_est4:*
14: gb_est5:*
15: em_estfun:*
16: em_estom:*
17: em_gss_hum:*
18: em_gss_inv:*
19: em_gss_pln:*
20: em_gss_vrt:*
21: em_gss_fun:*
22: em_gss_mam:*
23: em_gss_mus:*
24: em_gss_pro:*
25: em_gss_rod:*
26: em_gss_phg:*
27: em_gss_vrl:*
28: gb_gss1:*
29: gb_gss2:*
```

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	507.2	98.3	810	12	BG542554
2	492	95.3	834	10	BF679057
3	434.8	84.3	840	12	BG548515
4	420.2	81.4	760	12	BG542157

```

5 406.2 78.7 846 10 BF678252
6 333.6 64.7 818 10 BF677190
7 294 57.0 768 13 BQ573778
8 293.6 56.9 660 14 CF362072
9 250.8 48.6 652 13 BY752906
10 234 45.3 707 14 CA448745
11 228.6 44.3 712 14 CA419024
12 218.6 41.2 394 10 AW357271
13 198.8 38.5 669 10 AW612525
14 178.2 34.5 422 10 BF603113
15 175.6 34.0 403 14 CB768694
16 169 32.8 848 14 CB958187
17 167.8 32.5 1033 9 AL549464
18 167.8 32.5 1201 9 AL531122
19 166.2 32.2 874 14 CD244088
20 166.2 32.2 1201 9 AL514096
21 166.2 32.2 1201 13 BX399366
22 163 31.6 823 12 BI768140
23 161.4 31.3 987 13 BX45202
24 161.4 31.3 1201 13 BX402696
25 158.8 31.0 664 14 CB556672
26 159.4 30.9 651 14 CF363368
27 159 30.8 852 12 BI821954
28 156.6 30.3 528 14 CB152997
29 154.8 30.0 571 14 CD693938
30 154.6 30.0 640 9 AU137840
31 153.6 29.8 1201 9 AL558081
32 150.6 29.2 429 13 BY228345
33 148.8 28.8 551 12 BM364531
34 144.8 28.1 270 10 AW357272
35 143.6 27.8 812 13 BX378677
36 143.4 27.8 615 12 BM991911
37 141.8 27.5 411 10 BF902392
38 141.4 27.4 678 14 CB483332
39 140.8 27.3 403 13 BY228552
40 140.8 27.3 404 13 BY227642
41 140 27.1 373 13 BY041924
42 139 26.9 520 14 CB537050
43 138.6 26.9 449 10 BF932877
44 138.6 26.9 449 10 BF933349
45 137.2 26.6 1060 9 AL570702

```

ALIGNMENTS

```

RESULT 1
BG542554
LOCUS 602572052F1 NIH_MGC_77 Homo sapiens cDNA clone IMAGE:4696381 5',
DEFINITION mRNA sequence.
ACCESSION BG542554
VERSION BG542554.1 GI:13534787
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
REFERENCE 1 (bases 1 to 810)
AUTHORS NIH-MGC http://mgc.nci.nih.gov/.
TITLE National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL Unpublished (1999)
COMMENT Contact: Robert Strausberg, Ph.D.
Email: cgapbs@mail.nih.gov
Tissue Procurement: CLONTECH Laboratories, Inc.
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: LLC1523 row: h column: 14
High quality sequence stop: 667.

```

810 bp mRNA linear EST 03-APR-2001

Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

FEATURES
source

Location/Qualifiers
1. 810
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="IMAGE:4696381"
/clone="DH10B (T1 phage-resistant)"
/clone_lib="NIH MGC 77"
/note="Organ: lung; Vector: pDNR-LIB (Clontech); Site 1: SfiI (ggccattatgcc); Site 2: SfiI (ggccattatgcc); 5' and 3' adaptors were used in cloning as follows: 5' adaptor sequence: 5'-CACGCCATTATGCC-3' and 3' adaptor sequence: 5'-ATTCTAGAGCGCGGCGGCACATG-dt(30)BN-3' (where B = A, C, or G and N = A, C, G, or T). Average insert size 1.9 kb (range 0.5-4.0 kb). 12/15 colonies contained inserts by PCR. This library was enriched for full-length clones and was constructed by Clontech Laboratories (Palo Alto, CA). Note: this is a NIH_MGC Library."

ORIGIN

Query Match 98.3%; Score 507.2; DB 12; Length 810;
Best Local Similarity 99.4%; Pred. No. 8e-138;
Matches 509; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 GTCCCTCAGAACCTTAAGGTCCTTGAACCTCCATGGAATAGAAATTTAAAGGAGAG 60
DB 106 GTCCCTCAGAACCTTAAGGTCCTTGAACCTCCATGGAATAGAAATTTAAAGGAGAG 165
QY 61 AATGTGACTCTTACATGTAATGGGAACAATTTCTTGAAGTCAGTTCACCAATGGTTC 120
DB 166 AATGTGACTCTTACATGTAATGGGAACAATTTCTTGAAGTCAGTTCACCAATGGTTC 225
QY 121 CACATGCGACGCTTTTCAAGAGAGACAAATTCAGATTGTAATTTGTAATGCCAAATTT 180
DB 226 CACATGCGACGCTTTTCAAGAGAGACAAATTCAGATTGTAATTTGTAATGCCAAATTT 285
QY 181 GAAGACAGTGGAGAAATACAAATGTCAGACCAACAAAGTTAATGAGTGAACCTGTGTAC 240
DB 286 GAAGACAGTGGAGAAATACAAATGTCAGACCAACAAAGTTAATGAGTGAACCTGTGTAC 345
QY 241 CTGGAAGTCTTTCAGTGAAGTCTCTCTTCAAGGCTCTCTGTCAGGCTGATGGAGGC 300
DB 346 CTGGAAGTCTTTCAGTGAAGTCTCTCTTCAAGGCTCTCTGTCAGGCTGATGGAGGC 405
QY 301 CAGCCCTCTTTCAGTGAAGTCTCTCTTCAAGGCTCTCTGTCAGGCTGATGGAGGC 360
DB 406 CAGCCCTCTTTCAGTGAAGTCTCTCTTCAAGGCTCTCTGTCAGGCTGATGGAGGC 465
QY 361 TATAAGGATGTTGAAGTCTCTCAAGTCTGTTGAGAACCAACATCTCCATTACAAAT 420
DB 466 TATAAGGATGTTGAAGTCTCTCAAGTCTGTTGAGAACCAACATCTCCATTACAAAT 525
QY 421 GCCACAGTTGAAGACAGTGAAGTCTCTCAAGTCTGTTGAGAACCAACATCTCCATTACAAAT 480
DB 526 GCCACAGTTGAAGACAGTGAAGTCTCTCAAGTCTGTTGAGAACCAACATCTCCATTACAAAT 585
QY 481 GAGTCTGAGCCCTTCAACATTACTGTATAAAA 512
DB 586 GAGTCTGAGCCCTTCAACATTACTGTATAAAA 617

RESULT 2

BF679057
LOCUS 602153315F1 NIH_MGC_83 Homo sapiens cDNA clone IMAGE:4294467 5',
DEFINITION mRNA sequence.
ACCSSION BF679057
VERSION BF679057.1 GI:11952952
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

REFERENCE
AUTHORS
TITLE
JOURNAL
COMMENT

1 (bases 1 to 834)
NIH-MGC <http://mgi.mgi.nih.gov/>
National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
Email: cgapbs@mail.nih.gov
Tissue Procurement: CLONETECH Laboratories, Inc.
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:
<http://image.llnl.gov>
Plate: LLCM1143 row: n column: 04
High quality sequence stop: 621.

FEATURES
source

1. 834
Location/Qualifiers
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:4294467"
/lab_host="DH10B (T1 phage-resistant)"
/clone_lib="NIH MGC 83"
/note="Organ: prostate; Vector: pDNR-LIB (Clontech); Site 1: SfiI (ggccattatgcc); Site 2: SfiI (ggccattatgcc); 5' and 3' adaptors were used in cloning as follows: 5' adaptor sequence: 5'-CACGCCATTATGCC-3' and 3' adaptor sequence: 5'-ATTCTAGAGCGGCGGCACATG-dt(30)BN-3' (where B = A, C, or G and N = A, C, G, or T). Average insert size 1.4 kb (range 0.5-4.0 kb). 14/15 colonies contained inserts by PCR. This library was enriched for full-length clones and was constructed by Clontech Laboratories (Palo Alto, CA)."

ORIGIN

Query Match 95.3%; Score 492; DB 10; Length 834;
Best Local Similarity 99.6%; Pred. No. 2.4e-133;
Matches 514; Conservative 0; Mismatches 0; Indels 2; Gaps 2;

QY 1 GTCCCTCAGAACCTTAAGTCTCTTGAACCTCCATGGAATAGAAATTTAAAGGAGAG 60
DB 106 GTCCCTCAGAACCTTAAGTCTCTTGAACCTCCATGGAATAGAAATTTAAAGGAGAG 165
QY 61 AATGTGACTCTTACATGTAATGGGAACAATTTCTTGAAGTCAGTTCACCAATGGTTC 120
DB 166 AATGTGACTCTTACATGTAATGGGAACAATTTCTTGAAGTCAGTTCACCAATGGTTC 225
QY 121 CACATGCGACGCTTTTCAAGAGAGACAAATTCAGATTGTAATTTGTAATGCCAAATTT 180
DB 226 CACATGCGACGCTTTTCAAGAGAGACAAATTCAGATTGTAATTTGTAATGCCAAATTT 285
QY 181 GAAGACAGTGGAGAAATACAAATGTCAGACCAACAAAGTTAATGAGTGAACCTGTGTAC 240
DB 286 GAAGACAGTGGAGAAATACAAATGTCAGACCAACAAAGTTAATGAGTGAACCTGTGTAC 345
QY 241 CTGGAAGTCTTTCAGTGAAGTCTCTCTTCAAGGCTCTCTGTCAGGCTGATGGAGGC 300
DB 346 CTGGAAGTCTTTCAGTGAAGTCTCTCTTCAAGGCTCTCTGTCAGGCTGATGGAGGC 405
QY 301 CAGCCCTCTTTCAGTGAAGTCTCTCTTCAAGGCTCTCTGTCAGGCTGATGGAGGC 360
DB 406 CAGCCCTCTTTCAGTGAAGTCTCTCTTCAAGGCTCTCTGTCAGGCTGATGGAGGC 465
QY 361 TATAAGGATGTTGAAGTCTCTCAAGTCTGTTGAGAACCAACATCTCCATTACAAAT 420
DB 466 TATAAGGATGTTGAAGTCTCTCAAGTCTGTTGAGAACCAACATCTCCATTACAAAT 524
QY 421 GCCACAGTTGAAGACAGTGAAGTCTCTCAAGTCTGTTGAGAACCAAGTGTGGACGTGACTAT 480
DB 525 GCCACAGTTGAAGACAGTGAAGTCTCTCAAGTCTGTTGAGAACCAAGTGTGGACGTGACTAT 584
QY 481 GAGTCTGAGCCCTTCAACATTACTGTATAAAAAGCT 516

Db 585 GAGTCTGAG-CCTCACATTACTGTAAATAAGCT 619
|||||
RESULT 3
BG548515 840 bp mRNA linear EST 04-APR-2001
LOCUS 602576508F1 NIH_MGC_77 Homo sapiens cDNA clone IMAGE:4704624 5',
DEFINITION mRNA sequence.
ACCESSION BG548515
VERSION BG548515.1 GI:13547180
KEYWORDS Homo sapiens (human)
SOURCE
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 840)
REFERENCE NIH-MGC http://mgc.nci.nih.gov/.
AUTHORS National Institutes of Health, Mammalian Gene Collection (MGC)
TITLE Unpublished (1999)
JOURNAL
COMMENT Contact: Robert Strausberg, Ph.D.
Email: cgabs-r@mail.nih.gov
Tissue Procurement: CLONTECH Laboratories, Inc.
CDNA Library Preparation: CLONTECH Laboratories, Inc.
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: LLCM1544 row: p column: 01
High quality sequence stop: 590.
Location/Qualifiers
1. .840
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:4704624"
/lab_host="NIH_MGC_77"
/clone_lib="NIH_MGC_77"
/note="Organ: lung; Vector: pDNR-LIB (Clontech); Site: 1:
SfiI (ggccctcgcc); Site 2: SfiI (ggccattggcc); 5' and
3' adaptors were used in cloning as follows: 5' adaptor
sequence: 5'-CAGGCCATTATGGCC-3' and 3' adaptor sequence:
5'-ATTCTAGAGCGCGGCGGCACATG-dt(30)BN-3' (where B = A,
C, or G and N = A, C, G, or T). Average insert size 1.9
kb (range 0.5-4.0 kb). 12/15 colonies contained inserts
by PCR. This library was enriched for full-length clones
and was constructed by Clontech Laboratories (Palo Alto,
CA). Note: this is a NIH_MGC Library."

Query Match 84.3%; Score 434.8; DB 12; Length 840;
Best Local Similarity 96.9%; Pred. No. 1.7e-116;
Matches 465; Conservative 0; Mismatches 12; Indels 3; Gaps 2;
QY 1 GTCCCTCAGAAACCTTAGGCTCCTTGAACCCCTCATGGAATAGATATTTAAAGGAGAG 60
Db 106 GTCCCTCAGAAACCTTAGGCTCCTTGAACCCCTCATGGAATAGATATTTAAAGGAGAG 165
QY 61 AATGTGACTCTTACATGTAATGGGAACAATTTCTTGAAGTCAGTCCACCAATGGTTC 120
Db 166 AATGTGACTCTTACATGTAATGGGAACAATTTCTTGAAGTCAGTCCACCAATGGTTC 225
QY 121 CACATGGCAGCCTTTCAGAGAGACAAATTCAGATTTGAATTTGATGATGCCAAATTT 180
Db 226 CACATGGCAGCCTTTCAGAGAGACAAATTCAGATTTGAATTTGATGATGCCAAATTT 285
QY 181 GAAGACAGTGGAGAAATCAAAATGTCAGCACCACCAACCAAGTAAATGAGAGTGAACTGTGTAC 240
Db 286 GAAGACAGTGGAGAAATCAAAATGTCAGCACCACCAACCAAGTAAATGAGAGTGAACTGTGTAC 345
QY 241 CTGGAAGTCTTCAGTGAAGTCTGCTCTCAGCCCTCTGCTGAGGTGGTGTGAGGAGGC 300
|||||

Db 346 CTGGAAGTCTTCAGTGAAGTGGCTGCTCTCTCAGCCCTCTGCTGAGGTGGTATGGAGGC 405
QY 301 CAGCCCTCTCTCTCAGTGCCTGCTGTTGGAGAACTGGGATGTGTACAAGGTGATCTAT 360
Db 406 CAGCCCTCTCTCTCAGTGCCTGCTGTTGGAGAACTGGGATGTGTACAAGGTGATCTAT 465
QY 361 TATAAGGATGTGAAGTCTCAAGTACTGTATGAGAACACACACATCTCCATTACAAAT 420
Db 466 TATAAGGATGTGAAGTCTCAAGTACTGTATGAGAAACCAAAATCTCCATTACCAAT 525
QY 421 -GCCACAGTTGAAGACAGTGGAACTTAC-TACTGTACGGGCGGAAAGTGTGCAGCTGGAC 477
Db 526 TGCCACAGTTGAAGACAGTGGAACTTACTGTACGGGCGGAAAGTGTGCAGCTGGAC 585
BG542157 760 bp mRNA linear EST 03-APR-2001
LOCUS 602571381F1 NIH_MGC_77 Homo sapiens cDNA clone IMAGE:4695476 5',
DEFINITION mRNA sequence.
ACCESSION BG542157
VERSION BG542157.1 GI:13534390
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 760)
REFERENCE NIH-MGC http://mgc.nci.nih.gov/.
AUTHORS National Institutes of Health, Mammalian Gene Collection (MGC)
TITLE Unpublished (1999)
JOURNAL
COMMENT Contact: Robert Strausberg, Ph.D.
Email: cgabs-r@mail.nih.gov
Tissue Procurement: CLONTECH Laboratories, Inc.
CDNA Library Preparation: CLONTECH Laboratories, Inc.
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: LLCM1521 row: b column: 21
High quality sequence stop: 751.
Location/Qualifiers
1. .760
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:4695476"
/lab_host="NIH_MGC_77"
/clone_lib="NIH_MGC_77"
/note="Organ: lung; Vector: pDNR-LIB (Clontech); Site: 1:
SfiI (ggccctcgcc); Site 2: SfiI (ggccattggcc); 5' and
3' adaptors were used in cloning as follows: 5' adaptor
sequence: 5'-CAGGCCATTATGGCC-3' and 3' adaptor sequence:
5'-ATTCTAGAGCGCGGCGGCACATG-dt(30)BN-3' (where B = A,
C, or G and N = A, C, G, or T). Average insert size 1.9
kb (range 0.5-4.0 kb). 12/15 colonies contained inserts
by PCR. This library was enriched for full-length clones
and was constructed by Clontech Laboratories (Palo Alto,
CA). Note: this is a NIH_MGC Library."

Query Match 81.4%; Score 420.2; DB 12; Length 760;
Best Local Similarity 99.3%; Pred. No. 3.1e-112;
Matches 422; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
QY 92 TCTTTGAAGTCAATTCACCAATGTTCCCAATGGGAGCCCTTTCAGAGAGACAAATTT 151
Db 98 TGTAGCAGTCAATTCACCAATGTTCCCAATGGGAGCCCTTTCAGAGAGACAAATTT 157
QY 152 CAAATTTGAATTTGATGATGCCAAATTTGAAGACAGTGGAGATACAAATGTCAGCACC 211
Db 158 CAAATTTGAATTTGATGATGCCAAATTTGAAGACAGTGGAGATACAAATGTCAGCACC 217
|||||

QY 212 AACAAAGTTAATGAGAGTGAACCTGTGTACCTGGAGAGTCTTCAAGTCACTGGCTGCTCCTTC 271
 Db 218 AACAAAGTTAATGAGAGTGAACCTGTGTACCTGGAGAGTCTTCAAGTCACTGGCTGCTCCTTC 277
 QY 272 AGSCCTCTGCTGAGTGTGTATGAGAGGCGCCAGCCCTCTTCTCAGTGGCCATGGTTGGA 331
 Db 278 AGSCCTCTGCTGAGTGTGTATGAGAGGCGCCAGCCCTCTTCTCAGTGGCCATGGTTGGA 337
 QY 332 GGAACCTGGAGTGTATCAAGGTGATCTATTATAGAGTGGTGAAGCTCTCAAGTACTGGT 391
 Db 338 GGAACCTGGAGTGTATCAAGGTGATCTATTATAGAGTGGTGAAGCTCTCAAGTACTGGT 397
 QY 392 ATGAGAACCCACACATCTCCATTACAAATGCCACAGTTGAAGAGAGTGGAACTTACT 451
 Db 398 ATGAGAACCCACACATCTCCATTACAAATGCCACAGTTGAAGAGAGTGGAACTTACT 457
 QY 452 GTACGGGCAAGTGTGGCAGCTGAGTATGAGTCTGAGCCCTCAACATTACTGTATAA 511
 Db 458 GTACGGGCAAGTGTGGCAGCTGAGTATGAGTCTGAGCCCTCAACATTACTGTATAA 517
 QY 512 AAGCT 516
 Db 518 AAGCT 522
 RESULT 5
 BF678252
 LOCUS 602086161F1 NIH_MGC_83 Homo sapiens cDNA clone IMAGE:4250222 5',
 DEFINITION mRNA sequence.
 ACCESSION BF678252
 VERSION
 KEYWORDS
 SOURCE EST. GI:11952147
 ORGANISM Homo sapiens (human)
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 NIH-MGC http://mgi.nci.nih.gov/
 National Institutes of Health, Mammalian Gene Collection (MGC)
 Unpublished (1999)
 Contact: Robert Strausberg, Ph.D.
 Email: cgapbs-r@mail.nih.gov
 Tissue Procurement: CLONETECH Laboratories, Inc.
 cDNA Library Preparation: CLONETECH Laboratories, Inc.
 cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
 DNA Sequencing by: Incyte Genomics, Inc.
 Clone distribution: MGC clone distribution information can be
 found through the I.M.A.G.E. Consortium/LLNL at:
 http://image.llnl.gov
 Plate: LLCM1071 row: j column: 15
 High quality sequence stop: 609.
 Location/Qualifiers
 1..846
 /organism="Homo sapiens"
 /mol_type="mRNA"
 /db_xref="taxon:9606"
 /clone="IMAGE:4250222"
 /lab_host="DH10B (T1 phage-resistant)"
 /clone_lib="NIH_MGC_83"
 /note="Organ: prostate; Vector: pDNR-LTB (Clontech);
 Site1: SfII (ggcgcctcgcc); Site2: SfII
 (ggccattatggcc); 5' and 3' adaptors were used in cloning
 as follows: 5' adaptor sequence: 5'-CACGGCCATTATGGCC-3'
 and 3' adaptor sequence:
 5'-ATTCTAGAGCCGAGCGCGGCATG-dt(30)BN-3' (where B = A,
 C, or G and N = A, C, G, or T). Average insert size 1.4
 kb (range 0.5-4.0 kb). 14/15 colonies contained inserts
 by PCR. This library was enriched for full-length clones
 and was constructed by Clontech Laboratories (Palo Alto,
 CA)."
 FEATURES
 source
 1..846
 /organism="Homo sapiens"
 /mol_type="mRNA"

Query Match 78.7%; Score 406.2; DB 10; Length 846;
 Best Local Similarity 96.7%; Pred. No. 4.4e-108;
 Matches 500; Conservative 0; Mismatches 8; Indels 9; Gaps 8;
 QY 1 GTCCCTCAGAAACCTTAAGGTCTCTTGACCCCTCCATGGAATAGATATTAA-AGGAGA 59
 Db 100 GTCCCTCAGAAACCTTAAGGTCTCTTGACCCCTCCATGGAATAGATATTAA-AGGAGA 159
 QY 60 GAATGTGACTCTTACATGTAATGGGAACAATTTCTTTGAAAGTCACTTCCACCAATGGTT 119
 Db 160 GAATGTGACTCTTACATGTAATGGGAACAATTTCTTTGAAAGTCACTTCCACCAATGGTT 219
 QY 120 CCACAAATGGCAGCTTTTCAAGAGAGACAAATTCAGATTTGAATATTTGAAATGCCAAAT 179
 Db 220 CCACAAATGGCAGCTTTTCAAGAGAGACAAATTCAGATTTGAATATTTGAAATGCCAAAT 277
 QY 180 TGAAGACAGTGGAGAAATACAAATGTGAGCACCACAAAGTTAATGAGAGTGAACCTGTGTA 239
 Db 278 TGAAGACAGTGGAGAAATACAAATGTGAGCACCACAAAGTTAATGAGAGTGAACCTGTGTA 337
 QY 240 CTGGAAGTCTTCAAGTACTGGCTCTCTCAGCCCTCTGCTGAGTGGTGAATGGAGGG 299
 Db 338 CTGGAAGTCTTCAAGTACTGGCTCTCTCAGCCCTCTGCTGAGTGGTGAATGGAGGG 396
 QY 300 CCAGCCCTCTTCTCAGTGGCCATGGTTGGAGGAACCTGGGATGTACAGGGTGAATCTA 359
 Db 397 CCAGCCCTCTTCTCAGTGGCCATGGTTGGAGGAACCTGGGATGTACAGGGTGAATCTA 455
 QY 360 TTATAAGGATGGTGAAGCTCTCAAGTACTGATGAGAACCAACACATCTCCATTACAAA 419
 Db 456 TTATAAGGATGGTGAAGCTCTCAAGTACTGATGAGAACCAACAA-ATCTCCATTACAAA 513
 QY 420 TGCCACAGTTGAAGACAGTGGAACTACTGACGGGCAAGCTGGGAGCTGGACTA 479
 Db 514 TGCCACAG-TGAAGACAGTGGAACTACTGACGGGCAAGCTGGGAGCTGGACTA-GACTA 571
 QY 480 TGAGTCTGAGCCCTCAACATTACTGTATAATAAAGCT 516
 Db 572 TGAGTCTGAGCCCTCAACATTACTGTATAATAAAGCT 608
 RESULT 6
 BF677190
 LOCUS 602087255F1 NIH_MGC_83 Homo sapiens cDNA clone IMAGE:4251469 5',
 DEFINITION mRNA sequence.
 ACCESSION BF677190
 VERSION
 KEYWORDS
 SOURCE EST. GI:11951085
 ORGANISM Homo sapiens (human)
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 NIH-MGC http://mgi.nci.nih.gov/
 National Institutes of Health, Mammalian Gene Collection (MGC)
 Unpublished (1999)
 Contact: Robert Strausberg, Ph.D.
 Email: cgapbs-r@mail.nih.gov
 Tissue Procurement: CLONETECH Laboratories, Inc.
 cDNA Library Preparation: CLONETECH Laboratories, Inc.
 cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
 DNA Sequencing by: Incyte Genomics, Inc.
 Clone distribution: MGC clone distribution information can be
 found through the I.M.A.G.E. Consortium/LLNL at:
 http://image.llnl.gov
 Plate: LLCM1074 row: n column: 14
 High quality sequence stop: 616.
 Location/Qualifiers
 1..818
 /organism="Homo sapiens"
 /mol_type="mRNA"

```
/db_xref="taxon:9606"  
/clone="IMAGE:4251469"  
/lab_host="DH10B (T1 phase-resistant)"  
/clone_lib="NIH MGC_83"  
/note="Organ: prostate; Vector: pDNR-LIB (Clontech);  
Site 1: SfiI (ggcgccctggcc); Site 2: SfiI  
(ggcattatggcc); 5' and 3' adaptors were used in cloning  
as follows: 5' adaptor sequence: 5'-CACGCCATTATGGCC-3'  
and 3' adaptor sequence:  
5'-ATTCTAGAGCCGAGCGCCGACATG-dt(30)BN-3' (where B = A,  
C, or G and N = A, C, G, or T). Average insert size 1.4  
kb (range 0.5-4.0 kb). 14/15 colonies contained inserts  
by PCR. This library was enriched for full-length clones  
and was constructed by Clontech Laboratories (Palo Alto,  
CA)."
```

ORIGIN

```
Query Match 64.7%; Score 333.6; DB 10; Length 818;  
Best Local Similarity 89.6%; Pred. No. 1e-86;  
Matches 473; Conservative 0; Mismatches 39; Indels 16; Gaps 10;  
  
QY 1 GTCCCTCAGAACTTAAGTCTCTTGAACCCCTCCATGAATAGATATTTAAAGAGAG 60  
Db 110 GTCCCTCAGAACTTAAGTCTCTTGAACCCCTCCATGAATAGATATTTAAAGAGAG 169  
  
QY 61 AATGTGACTCTTACATGTAATGGGAACAATTTCTT-TGAAGTCAGTTCCACCAATGGTT 119  
Db 170 AATGTGACTCTTACATGTAATGGGAACAATTTCTTGTGAAGTCAGTTCCACCAATGGTT 229  
  
QY 120 CCAATATGGCAGCTTTCAGAGAGACAAATTCAGTTTGAATA----TTGTGAATGCCA 175  
Db 230 CCAATATGGCAGCTTTCAGAGAGACAAATTTCAAGTTTGTGAATTCAGTTTGAATGCCA 289  
  
QY 176 AAT--TTGAGAGACAGTGGAGAA--ACAATGTGAGCAGCAACCAAGTTAATGAGTGAAC 232  
Db 290 AATTTGAGAGACAGTGGAGAA--ACAATGTGAGCAGCAACCAAGTTAATGAGTGAAC 349  
  
QY 233 CTGTGACTTGAAGTCTTCAGTACGTGGCTGCTCCTCAGGCTCTGCTGAGTGGTGA 292  
Db 350 CTGTGACTTGAAGTCTTCAGTACGTGGCTGCTCCTCAGGCTCTGCTGAGTGGTGA 409  
  
QY 293 TGGAGGCCAGCCCTCTTCTCAGTGGCATGGTTGGAGGACTGGATGTGTAC-AAAG 351  
Db 410 TGGAGGCCAGCCCTCTTCTCAGTGGCATGGTTGGAGGACTGGATGTGTACAAAG 469  
  
QY 352 GTGATCTATTATAGAGTGTGAAGTCTCAAGTACTGTGTATGAGAACCAACATCTCC 411  
Db 470 GTGATCTATTATAGAGTGTGAAGTCTCAAGTACTGTGTATGAGAACCA-AAAATTTC 527  
  
QY 412 ATTACAAATGCCAGTGTGAAGACAGTGGAAACC---TACTACTGTAGCGGCAAA-GTGTG 467  
Db 528 ATTACAAATGCCAGTGTGAAGACAGGCGGAACCTAACTACTTGTACGGGCAAAAGGTGTG 587  
  
QY 468 GCAGTGGACTA-TGACTCTGAGCCCTCAACATTACTGTAAATAAAG 514  
Db 588 GCAGTGGACTATTGACTCTTGAGCCCTCAACATTACTGTAAATAAAG 635
```

RESULT 7

```
B0573778/c  
LOCUS B0573778 768 bp mRNA linear EST 19-JUN-2002  
DEFINITION UI-H-EZO-bav-1-04-0-UI.s1 NCI CGAP Ch1 Homo sapiens CDNA clone  
B0573778  
ACCESSION B0573778  
VERSION B0573778.1 GI:21477095  
KEYWORDS EST.  
SOURCE Homo sapiens (human)  
ORGANISM Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
1 (bases 1 to 768)  
REFERENCE NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.  
AUTHORS National Cancer Institute, Cancer Genome Anatomy Project (CGAP),  
TITLE
```

JOURNAL
COMMENT

Tumor Gene Index
Unpublished (1997)
Contact: Robert Strausberg, Ph.D.
Email: ccapbs@mail.nih.gov
Issue Procurement: Dr. Steven Gitelis/ Rush Presbyterian, Dept. of
Orthopedics
CDNA Library preparation: Dr. M. Bento Soares, University of Iowa
CDNA Library Arrayed by: Dr. M. Bento Soares, University of Iowa
CDNA Sequencing by: Dr. M. Bento Soares, University of Iowa
Clone Distribution: Clone distribution information can be obtained
from Dr. M. Bento Soares, bento-soares@uiowa.edu
The following repetitive elements were found in this cDNA
sequence: 1-41, >Alu1; 41-129, >Alu2 (matched complement)
93-129, >LINE2 (matched complement)
Seq primer: M13 FORWARD
POLYA-Yes.

FEATURES

Location/Qualifiers

```
1..768  
/organism="Homo sapiens"  
/mol_type="mRNA"  
/db_xref="taxon:9606"  
/clones="UI-H-EZO-bav-1-04-0-UI"  
/tissue_type="Chondrosarcoma Grade II"  
/dev_stage="Adult"  
/lab_host="DH10B (Life Technologies)"  
/clone_lib="NCI-CGAP Ch1"  
/note="Organ: Left Pelvis; Vector: p773-Pac (Pharmacia)  
with a modified polylinker; Site 1: EcoR I; Site 2: Not I;  
NCI CGAP Ch1 is a cDNA library containing the following  
tissue(s): Chondrosarcoma Grade II. The library was  
constructed according to Bonaldo, Lennon and Soares,  
Genome Research, 6:791-806, 1996. First strand cDNA  
synthesis was primed with an oligo-dT primer containing a  
Not I site. Double stranded cDNA was ligated to an EcoR I  
adaptor, digested with Not I, and cloned directionally  
into p773-Pac vector. The oligonucleotide used to prime  
the synthesis of first-strand cDNA contains a library tag  
sequence that is located between the Not I site and the  
dT18 tail. The sequence tag for this library is  
TGATCAGCT.  
TAG TISSUE=grade-2-chondrosarcoma  
TAG LIB=UI-H-EZO  
TAG_SEQ=ATCTAATATG"
```

ORIGIN

```
Query Match 57.0%; Score 294; DB 13; Length 768;  
Best Local Similarity 99.7%; Pred. No. 4.5e-75;  
Matches 294; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
  
QY 222 TGAGAGTGAACCTGTGTACCTGGAAGTCTTCAGTGAAGTGGTCTCTCAGGCTCTGC 281  
Db 768 TGAGAGTGAACCTGTGTACCTGGAAGTCTTCAGTGAAGTGGTCTCTCAGGCTCTGC 709  
  
QY 282 TGAGTGTGTATGAGGCGCAGCCCTCTTCTCAGTGGCATGGTTGAGGAACTGGGA 341  
Db 708 TGAGTGTGTATGAGGCGCAGCCCTCTTCTCAGTGGCATGGTTGAGGAACTGGGA 649  
  
QY 342 TGTGTACAGGTGATCTATTATTAAGATGGTGAAGCTCTCAAGTACTGTATGAGAACCA 401  
Db 648 TGTGTACAGGTGATCTATTATTAAGATGGTGAAGCTCTCAAGTACTGTATGAGAACCA 589  
  
QY 402 CAACATCTCCATTACAAATGCCACAGTTCAGACAGTGGAACTACTGTACGGGCAA 461  
Db 588 CAACATCTCCATTACAAATGCCACAGTTCAGACAGTGGAACTACTGTACGGGCAA 529  
  
QY 462 AGTGTGGCAGCTGGGACTATGAGTCTGAGCCCTCAACATTACTGTAAATAAAGCT 516  
Db 528 AGTGTGGCAGCTGGGACTATGAGTCTGAGCCCTCAACATTACTGTAAATAAAGCT 474
```

RESULT 8

```
CF362072  
LOCUS CF362072 660 bp mRNA linear EST 25-AUG-2003
```

```

DEFINITION      8284572 MARC 3P1G Sus scrofa cDNA 5', mRNA sequence.
ACCESSION       CF362072
VERSION         CF362072.1 GI:34161364
KEYWORDS        EST.
SOURCE          Sus scrofa (pig)
ORGANISM        Sus scrofa

REFERENCE
AUTHORS         Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
                 Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus.
TITLE           Smith, T.P.H., Freking, B.A., Ford, J.J., Valliet, J.L., Fox, J.,
                 Wise, T.A., Nomenan, D.J., Wray, J.B. and Keele, J.W.
                 A second set of porcine ESTs from a pooled-tissue normalized
                 library
JOURNAL          Unpublished (2003)
COMMENT         Contact: Smith TPL
                 USDA, ARS, US Meat Animal Research Center
                 PO Box 166, Clay Center, NE 68933-0166, USA
                 Tel: 402 762 4366
                 Fax: 402 762 4390
                 Email: smith@mail.marc.usda.gov
                 Single pass sequencing. Bases called with phred v0.020425.c and
                 trimmed with the aid of the trim.alt option. Vector identified with
                 cross_match v0.990329.
                 Plate: SRG8018 row: L column: 4
                 Seq primer: GTAATACGACTCACTATAGG.
FEATURES
source          1..660
                 /organism="Sus scrofa"
                 /mol_type="mRNA"
                 /db_xref="taxon:9823"
                 /tissue_type="pooled"
                 /lab_host="DH10B"
                 /clone_lib="MARC 3P1G"
                 /note="Vector: pcDNA3.1; Site 1: EcoRI; Site 2: NotI;
                 Library made with RNA pooled from multiple tissues
                 including brain, liver, muscle, placenta/endometrium,
                 ovary, testes, and bone marrow."

ORIGIN
Query Match      56.9%; Score 293.6; DB 14; Length 660;
Best Local Similarity 73.1%; Pred. No. 5.3e-75;
Matches 377; Conservative 0; Mismatches 139; Indels 0; Gaps 0;

QY      1  GTCCCTCAGAAACCTAGTCTCTTGAACCTCCATCGAATGAAATATTAAAGGAG 60
DB      91  GTCATCCAGGAATCTCAGGTGTCCTTGAATCCCATCGAATGGAATATTAGAGGAG 150
QY      61  AATGTGACTCTTACATGTAATGGGAAACAATTTCTTTGAAGTCAGTCCACCAATGGTTC 120
DB      151  AATGTGACTCTCATGTAATGGGAAAGATGCGCTTGAAATTTACCCCAATTTGACA 210
QY      121  CACAAATGGACCTTTTTCAGAGAGACAAATTCAGTTTGAATATTGTGAATGCCAAATTT 180
DB      211  CACAAACAAACAACTTTTGGAGAGTGAACAACTTCGAGTTGGACCTTAAGAAATGCAAAACCT 270
QY      181  GAGACAGTGGAGAAATCAATGTCAGCACCACACAGTTAATGAGAGTGAACCTGTGAC 240
DB      271  GGGACAGCGCAATACAGATGCCAAAGCAAGACTTTTACAATGAGTGAACCTGTGCAC 330
QY      241  CTGGAAGTCTTTCAGTGAAGTCTGCTCTTCAGGCGCTCTCTGAGGTGGTGTGATGGAGGC 300
DB      331  CTGAAGTCTATCAGTGAAGTCTGCTCTTCAGACCTCTGTCCCGGTGGTGGAGGAGGC 390
QY      301  CAGCCCTCTTCTCAGTGGCCATGGTTGAGAGAACTGGGATGTGTACAGGTGATCTAT 360
DB      391  CAGTCTCTCTCTCAGTGTGTCAGCGTGAAGAAATCTGAATGCTTATAGGTGATCTAC 450
QY      361  TATAAGGATGGTGAAGTCTCAAGTACTGTGTATGAGAACCAACATCTCCATTACAAAT 420
DB      451  TACAAGATGGCAAGCCCTCAGTACTGTGTATGAGAACCAACATCTCTCCATTACCAAT 510
QY      421  GCCACAGTTGAAGACAGTGAACCTTACTGTATGACGGGAAGAGTGGCAGCTGGACTAT 480

```

```

Db      511  GCCAAAAGAGAGACAGTGGCTCTTATTTGGTCACGGGCATTAATTCAAAAATACCAAA 570
QY      481  GAGTCTGAGCCCTCAACATTACTGTAAATAAAGCT 516
Db      571  AACTCTACTCTCACCATTACCAACACAGAT 606

RESULT 9
BY752906      652 bp mRNA linear EST 17-DEC-2002
LOCUS         BY752906 RIKEN full-length enriched, adult inner ear Mus musculus
DEFINITION    cDNA clone F930034C11 5', mRNA sequence.
ACCESSION     BY752906
VERSION       BY752906.1 GI:27184082
KEYWORDS      Mus musculus (house mouse)
SOURCE        Mus musculus
ORGANISM      Mammalia; Eutheria; Chordata; Craniata; Vertebrata; Euteleostomi;
                 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Muridae; Mus.
REFERENCE     1 (bases 1 to 652)
AUTHORS       Okazaki, Y., Furuno, M., Kasukawa, T., Adachi, J., Bono, H., Kondo, S.,
                 Nikaide, I., Oshino, N., Saito, R., Suzuki, H., Yamanaka, I.,
                 Kiyosawa, H., Yagi, K., Tomaru, Y., Hasegawa, Y., Nogami, A.,
                 Schonbach, C., Gojobori, T., Baidarelli, R., Hill, D.P., Sult, C.,
                 Hume, D.A., Quackenbush, J., Schriml, L.M., Kanapin, A., Matsuda, H.,
                 Batalov, S., Beisel, K.W., Blake, J.A., Bradt, D., Bruscia, V.,
                 Chothia, C., Corbani, L.E., Cousins, S., Della, B., Dragani, T.A.,
                 Fletcher, C.F., Forrest, A., Frazer, K.S., Gaasterland, I.,
                 Gariboldi, M., Gissi, C., Godzik, A., Gough, J., Grimmond, S.,
                 Gustincich, S., Hirokawa, N., Jackson, I.J., Jarvis, B.D., Kanai, A.,
                 Kawaji, H., Kawasawa, Y., Kedzierski, R.M., King, B.L., Konagaya, A.,
                 Kurochkin, I.V., Lee, Y., Lenhard, B., Lyons, P.A., Maglott, D.R.,
                 Maltais, L., Marchionni, L., McKenzie, L., Miki, H., Nagashima, T.,
                 Numata, K., Okido, T., Pavan, W.J., Pertea, G., Pesole, G.,
                 Petrovsky, N., Pillai, R., Pontius, J.U., Qi, D., Ramachandran, S.,
                 Ravasi, T., Reed, J.C., Reid, J., Reid, J., Ring, B.Z., Ringwald, M.,
                 Sandelin, A., Schneider, C., Semple, C.A., Setou, M., Shimada, K.,
                 Sultana, R., Takenaka, Y., Taylor, M.S., Teasdale, R.D., Tomita, M.,
                 Verardo, R., Wagner, L., Wahlestedt, C., Wang, Y., Watanabe, Y.,
                 Wells, C., Wilming, L.G., Wyszynski, B., Yang, Y., Yang, I.,
                 Yang, L., Yuan, Z., Zavolan, M., Zhu, Y., Zimmer, A., Carninci, P.,
                 Hayatsu, N., Hirozane-Kishikawa, I., Konno, H., Nakamura, M.,
                 Sakazume, N., Sato, K., Shiraki, T., Waki, K., Kawai, J., Aizawa, K.,
                 Arakawa, T., Fukuda, S., Hara, A., Hashizume, W., Imotani, K., Ishii, Y.,
                 Itoh, M., Kagawa, I., Miyazaki, A., Sakai, K., Sasaki, D., Shibata, K.,
                 Shinagawa, A., Yasunishi, A., Yoshino, M., Waterston, R., Lander, E.S.,
                 Rogers, J., Birney, E. and Hayashizaki, Y.
                 Analysis of the mouse transcriptome based on functional annotation
                 of 60,770 full-length cDNAs
                 Nature 420, 563-573 (2002)
                 22354683
                 12466851
Contact: Yoshihide Hayashizaki
Laboratory for Genome Exploration Research Group, RIKEN Genomic
Sciences Center (GSC), Yokohara Institute
The Institute of Physical and Chemical Research (RIKEN)
1-7-22 Suehiro-cho, Tsurumi-Ku, Yokohama, Kanagawa 230-0045, Japan
Tel: 81-45-503-9222
Fax: 81-45-503-9216
Email: genome-res@gsc.riken.go.jp,
URL: http://genome.ssc.riken.go.jp/
Adachi, J., Aizawa, K., Akimura, T., Arakawa, T., Carninci, P.,
Fukuda, S., Hashizume, W., Hayashida, K., Hirozane, T., Hori, F.,
Imotani, K., Ishii, Y., Itoh, M., Kagawa, I., Kawai, J., Kojima, Y.,
Kondo, S., Konno, H., Koya, S., Miyazaki, A., Murata, M., Nakamura, M.,
Nomura, K., Numazaki, R., Ohno, N., Ohsato, N., Saito, R., Sakazume, N.,
Sano, H., Sasaki, D., Sato, K., Shibata, K., Shiraki, T., Tagami, M.,
Takeda, Y., Waki, K., Watahiki, A., Muramatsu, M. and Hayashizaki, Y.
Direct Submission
Computational Analysis of Full-Length Mouse cDNAs Compared with
Human Genome Sequences Mamm. Genome. 12, 673-677 (2001)
Normalization and subtraction of cap-trapper-selected cDNAs to
prepare full-length cDNA libraries for rapid discovery of new

```


genes. Genome Res. 10 (10), 1617-1630 (2000)
 RIKEN integrated sequence analysis (RISA) system-384-format
 sequencing pipeline with 384 multicapillary sequencer. Genome Res.
 10 (11), 1757-1771 (2000)
 Computer-based methods for the mouse full-length cDNA
 encyclopedia: real-time sequence clustering for construction of a
 nonredundant cDNA library. Genome Res. 11 (2), 281-289 (2001)
 cDNA library was prepared and sequenced in Mouse Genome
 Encyclopedia Project of Genome Exploration Research Group in Riken
 Genomic Sciences Center and Genome Science Laboratory in RIKEN.
 Division of Experimental Animal Research in Riken contributed to
 prepare mouse tissues.
 Tissues were provided by Kirk W. Beisel (Boys Town National
 Research Hospital 555 North 30th Street Omaha, NE 68131 USA) whose
 assistance we gratefully acknowledge.
 Please visit our web site (<http://genome.gsc.riken.go.jp>) for
 further details.

FEATURES

source

```

1..652
  /organism="Mus musculus"
  /mol_type="mRNA"
  /strain="C57BL/6J"
  /db_xref="taxon:10090"
  /clone="F930034C11"
  /tissue_type="inner ear"
  /dev_stage="adult"
  /clone_lib="RIKEN full-length enriched, adult inner ear"

```

ORIGIN

```

Query Match      48.6%; Score 250.8; DB 13; Length 652;
Best Local Similarity 70.3%; Pred. No. 2.1e-62;
Matches 365; Conservative 0; Mismatches 148; Indels 6; Gaps 2;

QY 1 GPCCTCGAAGACCTTAAGGTCTCTTGAACCTCCATGGAATAGATATTAAGGAGAG 60
DB 102 GCCATGAGAAATCTGTACTACCTTGGACCCACATGGATTAGATATTACAGAGAG 151
QY 61 AATGTGACTCTTACATGTAATGGAACAATTTCTTTGAAGT---CAGTTCCACCAATGG 117
DB 162 AAAGTGACCTTCTCTGTCTGTTGGAACAATCACCTTCAATGAACCTACTACTAATGG 221
QY 118 TTCCCAATGGCAGCTTTTCAGAGAGACAAATTCAGTTTGAATTTGTAATGGCCAAA 177
DB 222 ATCCCAATGGTACCGTCTCTGAGTGAACTCTTCATTTGGTCATTTGAGTGCACC 281
QY 178 TTGGAAGACAGTGGAGAAATCAATGTGACACCAACAAGTTAATGAGAGTGAACCTGTG 237
DB 282 GTTCAAGACAGTGGAAATACATATGTGAGAAGCAAGATTGTTTAAGAGTAAACCTGTG 341
QY 238 TACCTGGAGTCTTCAGTGACTGCTCTCTCTCAGGCCTCTGCTGAGGTGGTGGAG 297
DB 342 TACTTGAATGTAAGCAAGATTGGCTGCTCTCTCAGACATCTGCTGACATGATCTTAGTC 401
QY 298 GGCCAGCCCTCTTCTCTCAGTGCCATGGTTGGAGGAACCTGGATGTTACAAAGGTGATC 357
DB 402 CATGGATCCTTTGACATCAGATGCCATGGCTGGGAAGAACTGGAATGTCCGCAAGGTGATC 461
QY 356 TATTATAGGATGGTGAAGCTCTCAAGTACTGGTATGAGAACCAACATCTCCATTACA 417
DB 462 TACTACAGAAATGACCATGCTTTCACTACATGATTATGAGAGCC---CCGTCCTCCATTAGA 518
QY 418 AATGCCACAGTTGAAGCAGTGGAACTTACTTGTACGGGCAAAAGTGTGGCAGCTGGAC 477
DB 519 GAGGCCACACTGAATGACAGTGGCACCTACCCTGNCAGGGCTATCTTAGGCAGGTGGAA 578
QY 478 TATGAGTCTGAGCCCTCAACATTTACTGTATATAAAGCT 516
DB 579 TATGAATCTGACAAATTCAGAAATTCGCTAGTAAAGCT 617

```

RESULT 10

CA448745/c

LOCUS

707 bp mRNA linear

EST 08-NOV-2002

DEFINITION

UI-H-E10-ayo-p-24-0-UI.s1 NCI CGAP E10 Homo sapiens cDNA clone
 UI-H-E10-ayo-p-24-0-UI 3', mRNA sequence.

ACCESSION

CA448745

VERSION

CA448745.1

KEYWORDS

EST.

SOURCE

Homo sapiens

ORGANISM

Homo sapiens (human)

REFERENCE

1 (bases 1 to 707)

AUTHORS

NCI-CGAP <http://www.ncbi.nlm.nih.gov/ncicgap>.

TITLE

National Cancer Institute, Cancer Genome Anatomy Project (CGAP),

JOURNAL

Tumor Gene Index

COMMENT

Unpublished (1997)

Contact: Robert Strausberg, Ph.D.

Email: cgaps-r@mail.nih.gov

Tissue Procurement: Dr. Jose Mercuende

cDNA Library Preparation: Dr. M. Bento Soares, University of Iowa

cDNA Library Arrayed by: Dr. M. Bento Soares, University of Iowa

DNA Sequencing by: Dr. M. Bento Soares, University of Iowa

Clone Distribution: Clone distribution information can be obtained

from Dr. M. Bento Soares, bento-soares@uiowa.edu

The following repetitive elements were found in this cDNA

sequence: 93-129, >LINE2 (matched complement)

Seq primer: M13 FORWARD

POLYA=Yes.

FEATURES

source

1..707

/organism="Homo sapiens"

/mol_type="mRNA"

/db_xref="taxon:9606"

/clones="UI-H-E10-ayo-p-24-0-UI"

/tissue_type="Chondrosarcoma"

/dev_stage="Adult"

/lab_host="DH10B (Life Technologies)"

/clone_lib="NCI-CGAP-E10"

/note="Organ: Left Pelvis; Vector: pT73-Pac (Pharmacia)

with a modified polylinker; Site 1: EcoR I; Site 2: Not I;

NCI CGAP E10 is a cDNA library containing the following

tissue(s): Chondrosarcoma. The library was constructed

according to Bonaldo, Lennon and Soares, Genome Research,

6:791-806, 1996. First strand cDNA synthesis was primed

with an oligo-dT primer containing a Not I site. Double

stranded cDNA was ligated to an EcoR I adaptor, digested

with Not I, and cloned directionally into pT73-Pac

vector. The oligonucleotide used to prime the synthesis of

first-strand cDNA contains a library tag sequence that is

located between the Not I site and the (dT)18 tail. The

sequence tag for this library is ACACTTGCAC.

TAG_TISSUE=chondrosarcoma

TAG_LIB=UI-H-E10

TAG_SEQ=ACACTTGCAC"

ORIGIN

```

Query Match      45.3%; Score 234; DB 14; Length 707;
Best Local Similarity 100.0%; Pred. No. 1.9e-57;
Matches 234; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 283 GAGTGTGATGAGGGCCAGGCCCTCTTCTCAGTGGCCATGGTTGGAGGAACCTGGAT 342
DB 707 GAGTGTGATGAGGGCCAGGCCCTCTTCTCAGTGGCCATGGTTGGAGGAACCTGGAT 648
QY 343 CTGTACAAAGGTGATCTATTATAGGATGGTGAAGCTCTCAAGTACTCTGGTATGAGAACCAC 402
DB 647 GTGTACAGGTGATCTATTATAGGATGGTGAAGCTCTCAAGTACTCTGGTATGAGAACCAC 588
QY 403 AACATCTCCATTACAAATGCCACAGTTGAAGACAGTGGAACTTACTTGTACGGCAAA 462
DB 587 AACATCTCCATTACAAATGCCACAGTTGAAGACAGTGGAACTTACTTGTACGGCAAA 528
QY 463 GTGTGGCAGCTGGACTATGATCTGAGCCCTCAACATTACTCTAATAAAGCT 516
DB 527 GTGTGGCAGCTGGACTATGATCTGAGCCCTCAACATTACTCTAATAAAGCT 474

```

RESULT 11
CA419024/c
LOCUS
DEFINITION
ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM
REFERENCE
AUTHORS
TITLE
JOURNAL
COMMENT

CA419024
UI-H-E21-bbj-e-19-0-UI-s1 NCI CGAP Ch2 Homo sapiens CDNA clone
UI-H-E21-bbj-e-19-0-UI 3', mRNA sequence.
CA419024
CA419024.1 GI:24781675
EST.
Homo sapiens (human)
Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 712)
NCI-CGAP <http://www.ncbi.nlm.nih.gov/ncicgap>.
National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
Tumor Gene Index
Unpublished (1997)
Contact: Robert Strausberg, Ph.D.
Email: cgapsb-remail.nih.gov
Tissue Procurement: Dr. Steven Gitelis/ Rush Presbyterian, Dept. of
Orthopaedics
CDNA Library preparation: Dr. M. Bento Soares, University of Iowa
CDNA Library Arrayed by: Dr. M. Bento Soares, University of Iowa
DNA Sequencing by: Dr. M. Bento Soares, University of Iowa
Clone Distribution: Clone distribution information can be obtained
from Dr. M. Bento Soares, bento-soares@uiowa.edu
The following repetitive elements were found in this CDNA
sequence: 1-42, >(TAAA)nSimple_repeat (matched complement)
94-130, >LINE2, (matched complement)
Seq primer: M13 FORWARD
POLYA=Yes.

FEATURES
source
1..712
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="UI-H-E21-bbj-e-19-0-UI"
/tissue_type="Chondrosarcoma Grade II"
/dev_stage="Adult"
/lab_host="DH10B (Life Technologies)"
/clone_lib="NCI CGAP Ch2"
/note="Organ: Left Pelvis; Vector: pT73-Pac (Pharmacia)
with a modified polylinker; Site 1: EcoR I; Site 2: Not I;
NCI CGAP Ch2 is a normalized CDNA library containing the
following tissue(s): Chondrosarcoma Grade II. The library
was constructed according to Bonaldo, Lennon and Soares,
Genome Research, 6:791-806, 1996. First strand cDNA
synthesis was primed with an oligo-dT primer containing a
Not I site. Double stranded cDNA was ligated to an EcoR I
adaptor, digested with Not I, and cloned directionally
into pT73-Pac vector. The oligonucleotide used to prime
the synthesis of first-strand cDNA contains a library tag
sequence that is located between the Not I site and the
(dT)18 tail. The sequence tag for this library is
TGATCAGCT.
TAG_TISSUE=grade-2-chondrosarcoma
TAG_LIB=UI-H-E21
TAG_SEQ=ATCTAATATG

ORIGIN
Query Match 44.3%; Score 228.6; DB 14; Length 712;
Best Local Similarity 97.1%; Pred. No. 7.6e-56;
Matches 231; Conservative 0; Mismatches 7; Indels 0; Gaps 0;

QY 399 CCACAACTCTCCATTACAAATGCCACAGTTGAAGACAGTGAACCTACTACTGTACGGG 458
|||||
Db 592 CCACAACTCTCCATTACAAATGCCACAGTTGAAGACAGTGAACCTACTACTGTACGGG 533
|||||
QY 459 CAAAGTGTGGCAGCTGGACTATGAGTCTGAGCCCTCACACATTACTGTAAATAAAGCT 516
|||||
Db 532 CAAAGTGTGGCAGCTGGACTATGAGTCTGAGCCCTCACACATTACTGTAAATAAAGCT 475
|||||

RESULT 12
AW357271
LOCUS
DEFINITION
ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM
REFERENCE
AUTHORS
TITLE
JOURNAL
MEDLINE
PUBMED
COMMENT

AW357271
40240 MARC 2BOV Bos taurus CDNA 5', mRNA sequence.
AW357271
AW357271.1 GI:6861277
EST.
Bos taurus (cow)
Bos taurus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
Bovidae; Bovinae; Bos.
1 (bases 1 to 394)
Smith, T.P.D., Grosse, W.M., Freking, B.A., Roberts, A.J., Stone, R.T.,
Casas, E., Wray, J.E., White, J., Cho, J., Fahrenkrug, S.C.,
Benzett, G.L., Heaton, M.P., Laegreid, W.M., Rohrer, G.A.,
Chitko-McKown, C.G., Pettea, G., Holt, I., Karamycheva, S., Liang, F.,
Quackenbush, J. and Keefe, J.W.
Sequence evaluation of four pooled-tissue normalized bovine CDNA
libraries and construction of a gene index for cattle
Genome Res. 11 (4), 626-630 (2001)
21180013
11282978
Contact: Smith TPL
USDA, ARS, US Meat Animal Research Center
PO Box 166, Clay Center, NE 68933-0166, USA
Tel: 402 762 4366
Fax: 402 762 4390
Email: smith@email.marc.usda.gov
Single pass sequencing. Bases called and trimmed with phred
v0.980904.e. Vector identified by cross_match with the -minscore 20
and -minmatch 12 options.
PCR Primers
FORWARD: AGGAACACAGTATGACCAT
BACKWARD: GTTTCCTCCAGTCACGAG
Plate: 18 row: C column: 5
Seq primer: ATTGAGTGACACTATAG.
Location/Qualifiers
1..394
/organism="Bos taurus"
/mol_type="mRNA"
/db_xref="taxon:9913"
/tissue_type="pooled"
/lab_host="DH10B"
/clone_lib="MARC 2BOV"
/note="Vector: pCMV SPORT6; Site 1: NotI; Site 2: SalI;
Library made from pooled tissue from testis, thymus,
semitendinosus muscle, longissimus muscle, pancreas,
adrenal, and endometrium."

ORIGIN
Query Match 41.2%; Score 212.6; DB 10; Length 394;
Best Local Similarity 73.3%; Pred. No. 2.6e-51;
Matches 272; Conservative 0; Mismatches 99; Indels 0; Gaps 0;

QY 279 TGCTAGGTGGTATGAGGGCCAGCCCTCTTCCTCAGTGCCATGGTTGGAGGAATG 338
Db 712 TGCTAGGTGGTATGAGGAGCCAGCCCTCTTCCTCAGTGCCATGGTTGGAGGAATG 653
QY 339 GGATGTGTACAAGGTATCTATTATAGGATGGTGAAGCTCTCAAGTACTGGTATGAGAA 398
Db 652 GGATGTGTACAAGGTATCTATTATAGGATGGTGAAGCTCTCAAGTACTGGTATGAGAA 593

QY 129 CAGCCTTTTCAAGAGACAAATTCAGTTTGAATATTTGTAATGCCAAATTCAGAGACAG 188
 DB 144 AACAGATTTCACAGATATATTCAGATGCGACATTTGTAAGAGCAGCGATGCGAGACAG 203
 QY 189 TGGAGAAATACAAATGTGAGCAGCAACCAAGTTAATGAGAGTGAACCTGTGTACCTGGAAGT 248
 DB 204 TGGGGAATACCAATGCGCAATCAAGGATTTGCCATCAGTGAACCCGTATACCTAATGT 263
 QY 249 CTTAGTACCTGGTGTCTCTTCAAGGCTCTCTGAGGTTGATGAGGCGCCAGCCCT 308
 DB 264 CATCAGTACCTGGTGTATCATTCATCAGGCTCTCTGAGGTTGATGAGGCGCTCCCT 323
 QY 309 CTTCTCAGTGGCCATGTTTGGAGGAACTGGGATGTGTACAAAGTGATCTATTATTAAGGA 368
 DB 324 CTTCTCAGTGGCCACAGTTGAGAGATCTGAATGTTCTCAGGTGATCTACTACAAGGA 383
 QY 369 TGGTGAAGCTC 379
 DB 384 TAACAAGCTC 394

RESULT 13
 LOCUS AW612525 669 bp mRNA linear EST 23-MAR-2000
 DEFINITION hh03f07.x1 NCI CGAP Kid11 Homo sapiens cDNA clone IMAGE:2954053 3' similar to gb:X06948 HIGH AFFINITY IMMUNOGLOBULIN EPSILON RECEPTOR ALPHA-SUBUNIT (HUMAN); mRNA sequence.
 ACCESSION AW612525
 VERSION AW612525.1 GI:7317711
 KEYWORDS Homo sapiens (human)
 SOURCE Homo sapiens

REFERENCE
 AUTHORS Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 1 (bases 1 to 669)
 TITLE NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
 JOURNAL National Cancer Institute, Cancer Genome Anatomy Project (CGAP), Tumor Gene Index
 COMMENT Unpublished (1997)
 CONTACT: Robert Strauberg, Ph.D.
 EMAIL: cgapbs-remail.nih.gov
 Tissue Procurement: Christopher Moskaluk, M.D., Ph.D., Michael R. Emmert-Buck, M.D., Ph.D.
 cDNA Library Preparation: M. Bento Soares, Ph.D.
 DNA Library Arrayed by: Greg Lennon, Ph.D.
 Cloning Distribution: Washington University Genome Sequencing Center
 Cloning Distribution: NCI-CGAP clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at: image.llnl.gov/image/html/iresources.shtml
 Seq primer: -40up from Gibco
 High quality sequence stop: 438.

FEATURES
 source
 1..669
 /organism="Homo sapiens"
 /mol_type="mRNA"
 /db_xref="taxon:9606"
 /clone="IMAGE:2954053"
 /lab_host="DH10B"
 /clone_lib="NCI CGAP Kid11"
 /note="Organ: Kidney; Vector: p773D-Pac (Pharmacia) with a modified polylinker; Site: Not 1; Site 2: Eco RI; Plasmid DNA from the normalized library NCI CGAP Kid3 was prepared, and ss circles were made in vitro. Following HAP purification, this DNA was used as tracer in a subtractive hybridization reaction. The driver was PCR-amplified cDNAs from a pool of 5,000 clones made from the same library (clonerDs 1322376-1323911, 1456007-1456775, and 1500552-1502855). Subtraction by Bento Soares and M. Fatima Bonaldo."

ORIGIN
 Query Match 38.5%; Score 198.8; DB 10; Length 669;
 Best Local Similarity 96.2%; Pred. No. 4.3e-47;
 Matches 245; Conservative 0; Mismatches 93; Indels 1; Gaps 1;

Matches 203; Conservative 0; Mismatches 8; Indels 0; Gaps 0;
 QY 306 CCTCTTCTCAGGTGCCATGTTTGGAGAACTGGGATGTGTACAAAGTGATCTATTATAA 365
 DB 669 CCTCTTCTCAGGTGCCATGTTTGGAGAACTGGGATGTGTACAAAGTGATCTATTATAA 610
 QY 366 GGATGGTGAAGCTCTCAAGTACTGGTATGAGACCAACACATCTCCATTACAAATGCCAC 425
 DB 609 GGATGGTGAAGCTCTCAAGTACTGGTATGAGACCAACACATCTCCATTACATATGCCAC 550
 QY 426 AGTTGAAGACAGTGGAACTTACTTACTGTCAGGCAAAAGTGTGGCAGCTGGAGTATGAGTC 485
 DB 549 AGTTGAAGACAGTGGAACTTACTTACTGTCAGGCAAAAGTGTGGCAGCTGGAGTATGAGTC 490
 QY 486 TGAGCCCTCTCAACATTTACTCTTAATAAAGCT 516
 DB 489 TGAGCCCTCTCAACATTTACTCTTAATAAAGCT 459

RESULT 14
 LOCUS BF603113 422 bp mRNA linear EST 25-APR-2001
 DEFINITION 268539 MARC 3BOV Bos taurus cDNA 5', mRNA sequence.
 ACCESSION BF603113
 VERSION BF603113.1 GI:11700395
 KEYWORDS EST.
 SOURCE Bos taurus (cow)
 ORGANISM Bos taurus

REFERENCE
 AUTHORS Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae; Bovidae; Bos.
 1 (bases 1 to 422)
 TITLE Smith, T.P.L., Grosse, W.M., Freking, B.A., Roberts, A.J., Stone, R.T., Casas, E., Wray, J.E., White, J., Cho, J., Fahrnerkrug, S.C., Bennett, G.L., Heaton, M.P., Laegreid, W.W., Rohrer, G.A., Chitko-Mckown, C.G., Berdea, G., Holt, I., Karamycheva, S., Liang, F., Quackenbush, J. and Keesle, J.W.
 Sequence evaluation of four pooled-tissue normalized bovine cDNA libraries and construction of a gene index for cattle
 Genome Res. 11 (4), 626-630 (2001)

JOURNAL 21180013
 MEDLINE 11282978
 PUBMED
 COMMENT Contact: Smith TPL
 USDA, ARS, US Meat Animal Research Center
 PO Box 166, Clay Center, NE 68933-0166, USA
 Tel: 402 762 4366
 Fax: 402 762 4390
 Email: smith@email.marc.usda.gov
 Single pass sequencing. Bases called and alt trimmed with phred v0.980904.e. Vector identified by cross_match with the -minscore 18 and -minmatch 12 options.

PCR Primers
 FORWARD: AGGAACACAGCTATGACCAT
 BACKWARD: GTTTCCTCCAGTCACGACG
 Plate: 47 row: N column: 12
 Seq primer: ATTAGTGACACTATAG.

FEATURES
 source
 1..422
 /organism="Bos taurus"
 /mol_type="mRNA"
 /db_xref="taxon:9913"
 /tissue_type="pooled"
 /lab_host="DH10B"
 /clone_lib="MARC 3BOV"
 /note="Vector: pCMV SPORT6; Site 1: NotI; Site 2: SalI; Library made from pooled tissue from marrow, alveolar macrophage, ovary, fetal semitendinosus muscle, and fetal longissimus muscle."

ORIGIN
 Query Match 34.5%; Score 178.2; DB 10; Length 422;
 Best Local Similarity 72.3%; Pred. No. 3.7e-41;
 Matches 245; Conservative 0; Mismatches 93; Indels 1; Gaps 1;

QY 9 GAACCTAAGGTCTCTTGAACCTCCATG-GAATAGAAATATTTAAAGGAGAGAAATGTGA 67
 DB 84 GAAATCTAAGGGTCTCTTGAATCCACCATGAGAGAAATATCTTAAAGGAGAGATCTGTGA 143
 QY 68 CTCTTACATGTAATGGGAACAATTTCTTTGAAGTCAGTTCCACCAATGGTTCCACAATG 127
 DB 144 CTCCTTACATGGTACGAATGGTTCTCTGAGACCACTCTCTCTGTGGNATCCCAATG 203
 QY 128 GCAGCCTTTGAGAGAGACAATTCAGTTTGAATATGTGAATGCCAAATTTGAAGACA 187
 DB 204 GAACAGTTTTCACACGAATATTCAGATGCCCAATTTGAAAGCAGCATGTCAGGACA 263
 QY 188 GTGGAGAATACAAATGTGAGACCAACCAAGTTAATGAGAGTGAACCTGTGTACCTGGAAG 247
 DB 264 GTGGGATACCAATGCCGATCAAGGATTGCCATCAGTGAACCCGTATACCTAATG 323
 QY 248 TCTTCAGTGAATGGTGTCTCTTCAAGCCTCTGTGAGGTGTGTGATGAGGGCCAGGCC 307
 DB 324 TCATCAGTGAATGGTGTGATCATTCAGGCCTCTGTGAGGTGATGATGAGGGTGAGTCCC 383
 QY 308 TCTTCTCAGTGCATGTTGGAGGACTGGGATGTCT 346
 DB 384 TCTTCTCAGTGCACACAGTTGGAAGATCTGAATGTCT 422

RESULT 15
 LOCUS CB768694 403 bp mRNA linear EST 16-MAY-2003
 DEFINITION AMGNNUC:SRPB2-00228-E10-A srpb2 (10220) Rattus norvegicus cDNA
 clone srpb2-00228-e10 5', mRNA sequence.
 ACCESSION CB768694
 VERSION CB768694.1 GI:29857085
 KEYWORDS EST.
 ORGANISM Rattus norvegicus (Norway rat)
 Rattus norvegicus
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
 Rattus.
 1 (bases 1 to 403)
 REFERENCE 1
 AUTHORS Angen EST Program.
 TITLE Angen Rat EST Program
 JOURNAL Unpublished (2003)
 COMMENT Contact: Dan Fitzpatrick
 Angen, Inc
 One Angen Center Drive, Thousand Oaks, CA 91320-1799, USA
 Tel: 805 447-4881
 Plate: 00228 row: e column: 10.
 FEATURES
 Location/Qualifiers
 1..403
 /organism="Rattus norvegicus"
 /mol_type="mRNA"
 /db_xref="taxon:10116"
 /clone="srpb2-00228-e10"
 /tissue_type="prostate tissue"
 /clone_lib="srpb2 (10220)"
 /note="Vector: pSPORT1; Site_1: SalI; Site_2: NotI; rat
 prostate normalized double selected poly(A+) mRNA size
 fraction > 1 kb"

ORIGIN

Query Match 34.0%; Score 175.6; DB 14; Length 403;
 Best Local Similarity 69.9%; Pred. No. 2.1e-40;
 Matches 235; Conservative 0; Mismatches 101; Indels 0; Gaps 0;
 QY 181 GAAGACAGTGGAGAAATACAAATGTGACGACCAACAAAGTTAATGAGAGTGAACCTGTGTAC 240
 DB 11 GAAGACAGTGGAAATATACATATGTGAGAGCAAGGATTTTAAAGAGCAACCTGTGTAC 70
 QY 241 CTGGAAGTCTTCAGTACGTGGTCTCTTCAGGCTCTGAGGTGGTGTGAGGGGC 300
 DB 71 TTGAACNTGATGANGAGTGGTCTGTCTCCAAATCTTCTGCTGACGTGCTTAGACAAT 130

QY 301 CAGCCCTCTTCTCAGGTGCCATGGTTGAGGAACTGGGATGTGTACAAGGTGATCTAT 360
 DB 131 GGATCCTTTTGACATCAGATGCGGTAGCTGGAAGAAATGGAAGTCCACAAGGTGATCTAC 190
 QY 361 TATAAGGATGGTGAAGCTCTCAAGTACTGGTATGAGAACCAACAACATCTCCATTACAAAT 420
 DB 191 TACAGGACGACATTTGCTTTCAAGTACTCTTATGACGCAACAACATCTCCATTAGAAG 250
 QY 421 GCCACAGTTGAAGACAGAGTGGAACCTACTACTGTACGGGCAAAAGTGTGGCAGCTGGACTAT 480
 DB 251 GCCACATTTAATGACAGTGGCAGCTACCACTGCACAGGCTATTTTGAACAAGTTGAATGT 310
 QY 481 GAGTCTGAGCCCTCAACATTTACTGTATAATAAAGCT 516
 DB 311 AAATCTGATAAATTCAGTATTCTGTAGTAAAGAT 346

Search completed: October 10, 2004, 19:44:40
 Job time : 1742.12 secs

GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.

OM protein - protein search, using sw model

Run on: October 6, 2004, 08:59:38 ; Search time 38.8904 Seconds
(without alignments)
1249.617 Million cell updates/sec

Title: US-10-763-400-13

Perfect score: 947

Sequence: 1 VPQKPKVSLNPNWIFKGE.....GKWWQDYSEBLNITVIKA 172

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1586107 seqs, 282547505 residues

Total number of hits satisfying chosen parameters: 1586107

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

1: Geneseqp_29Jan04:*
2: Geneseqp1980s:*
3: Geneseqp1990s:*
4: Geneseqp2000s:*
5: Geneseqp2001s:*
6: Geneseqp2002s:*
7: Geneseqp2003as:*
8: Geneseqp2003bs:*
9: Geneseqp2004s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	947	100.0	172	2 AAY33185	Aay33185 Human SFC
2	947	100.0	172	3 AAY94211	Aay94211 Human PhF
3	947	100.0	172	3 AAB31587	Aab31587 A Fc epsi
4	947	100.0	176	3 AAY94210	Aay94210 Human PhF
5	947	100.0	176	4 AAG65597	Aag65597 Amino aci
6	947	100.0	182	3 AAY96234	Aay96234 Recombina
7	947	100.0	183	3 AAY96232	Aay96232 Recombina
8	947	100.0	197	2 AAR45778	Aar45778 Human diH
9	947	100.0	197	4 AAB31586	Aab31586 A Fc epsi
10	947	100.0	232	2 AAB31585	Aab31585 Amino aci
11	947	100.0	235	2 AAR26064	Aar26064 Human FcE
12	947	100.0	257	1 AAR90385	Aap90385 Alpha sub
13	947	100.0	257	2 AAR05025	Aar05025 Alpha sub
14	947	100.0	257	2 AAR14772	Aar14772 Human Fc(
15	947	100.0	257	2 AAR42336	Aar42336 Human Fce
16	947	100.0	257	2 AAW24066	Aaw24066 Alpha sub
17	947	100.0	257	2 AAW61190	Aaw61190 The alpha
18	947	100.0	257	2 AAW48094	Aaw48094 Human IGE
19	947	100.0	257	4 AAB74667	Aab74667 Human imm
20	947	100.0	257	4 AAB31584	Aab31584 Amino aci
21	947	100.0	257	5 AAG32801	Aag32801 Human IGE
22	947	100.0	257	6 ABO01301	Abo01301 Human pro
23	947	100.0	257	7 ABE85536	Abe85536 Human imm
24	947	100.0	257	7 ADD48674	Add48674 Human Pro
25	947	100.0	260	3 AAY96230	Aay96230 Human Fc

26 947 100.0 635 4 AAB31594
27 947 100.0 660. 4 AAB31593
28 947 100.0 731. 4 AAB31591
29 947 100.0 756. 4 AAB31590
30 947 100.0 978. 2 AAW48096
31 947 100.0 978. 5 AAG32803
32 931 98.3 193. 2 AAR9281
33 922 97.4 176. 4 AAG65598
34 851 89.9 247. 2 AAR30483
35 775 81.8 281. 2 AAR13867
36 714.5 75.4 218. 6 ABO01302
37 679 71.7 281. 2 AAR13870
38 639 67.5 281. 2 AAR13872
39 606 64.0 281. 2 AAR13869
40 570 60.2 201. 2 AAY27061
41 570 60.2 236. 2 AAY27060
42 570 60.2 255. 2 AAY27058
43 564 59.6 190. 5 AAE18631
44 522 55.1 199. 2 AAW81111
45 516 54.5 197. 2 AAW81115

ALIGNMENTS

RESULT 1
AAY33185
ID AAY33185 standard; protein; 172 AA.
XX
AC AAY33185;
XX
DT 15-NOV-1999 (first entry)
XX
DE Human sFc-epsilonRI protein fragment.
XX
KW Fc receptor; Fc-gammaRIIa; human; FCR; model; three-dimension; 3-D;
KW atomic coordinate; bioactive compound design; computer-assisted;
KW drug design; therapy; inhibitor; Fc-gammaR; Fc-epsilonRI; IGG; IGE;
KW tissue damage; hypersensitivity; inflammatory cell recruitment;
KW inflammatory modulator; Fc-gammaRIa; immune function regulation;
KW anti-inflammatory; immunoprotective.
XX
OS Homo sapiens.
XX
FN WO9940117-Al.
XX
PD 12-AUG-1999.
XX
PF 04-FEB-1999; 99WO-IB000367.
XX
PR 06-FEB-1998; 98US-0073972P.
PR 11-SEP-1998; 98US-0099994P.
XX
PA (ILEX-) ILEXUS PTY LTD.
XX
PI Hogarth PM, Powell MS, McKenzie IFC, Maxwell KF, Garrett TPJ;
PI Epa V, Baill JB, Matthews BR, McCarthy TD, Pietersz GA;
XX
PS WPI; 1999-539978/45.
XX
PT Three-dimensional structures and models of Fc receptors, useful in
PT computer-assisted drug design.
XX
PS Claim 11; Page 318-319; 326pp; English.

XX This invention describes a novel model of an Fc receptor (FcR) protein
XX representing a three-dimensional (3-D) structure that substantially
XX conforms to the specified atomic coordinates. Computer model images of
XX the FcR can be used to design bioactive chemical compounds, e.g.
XX oligonucleotides, peptides, peptidomimetics and small organic molecules,
XX by computer-assisted methods of drug design. Therapeutic compositions
XX that inhibit the activity of Fc-gammaR or Fc-epsilonRI can be used to
XX reduce IgG- or IgE-mediated tissue damage, e.g. IgG- or IgE-mediated

CC hypersensitivity, recruitment of inflammatory cells or release of
 CC inflammatory modulators. The therapeutic compositions can also be used to
 CC treat disease in animals. The knowledge of the 3-D structure of Fc-gamma
 CC R1a and models of other FcR provides a means for designing and producing
 CC compounds that regulate immune function and inflammation in an animal,
 CC including humans (i.e. structure based drug design). For example,
 CC chemical compounds can be designed to block binding of immunoglobulin to
 CC an Fc receptor protein using various computer programs and models. The
 CC products of the invention have anti-inflammatory and immunoprotective
 CC activity. This sequence represents the human sFc-epsilonRI protein
 CC fragment described in the method of the invention
 XX
 XX

XX Sequence 172 AA;

Query Match 100.0%; Score 947; DB 2; Length 172;
 Best Local Similarity 100.0%; Pred. No. 4.1e-66;
 Matches 172; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 VPQKPKVSLNPPNRIKGENVTLTCNGNPFVSSSTKWFHNGSLSEETNSLIVNAKF 60
 Db 1 VPQKPKVSLNPPNRIKGENVTLTCNGNPFVSSSTKWFHNGSLSEETNSLIVNAKF 60
 QY 61 EDGGEYKCHQOVNESEPVYLEVSDMLLQASAEVWMEGQPLFRLCHGWNWDVYKVIY 120
 Db 61 EDGGEYKCHQOVNESEPVYLEVSDMLLQASAEVWMEGQPLFRLCHGWNWDVYKVIY 120
 QY 121 YKDGALKYWEHNHISITNATVEDSGTYCTGKQWQLDYSEPLNITVIKA 172
 Db 121 YKDGALKYWEHNHISITNATVEDSGTYCTGKQWQLDYSEPLNITVIKA 172

RESULT 2

AA94211

ID AA94211 standard; protein; 172 AA.

AC AA94211;

XX

DT 01-AUG-2000 (first entry)

XX Human PhFcepsilonRIalpha 1-172.

DE Protein co-ordinate data; PhFcepsilonRIalpha 1-172; FcR;

XX FcepsilonRIalpha 1-172; antibody Fc receptor; allergy;

KW anaphylactic shock.

XX Homo sapiens.

OS

XX

XX

XX

XX

XX

XX

XX

XX

XX

XX

XX

XX

XX

XX

XX

XX

XX

XX

XX

XX

XX

XX

XX

XX

XX

FT Region /label= beta_sheet_secondary_structure
 FT 135..139
 FT /label= beta_sheet_secondary_structure
 FT 147..155
 FT /label= beta_sheet_secondary_structure
 FT 158..170
 FT /label= beta_sheet_secondary_structure
 XX
 XX WO200026246-A2.

XX 11-MAY-2000.

XX 05-NOV-1999; 99WO-US026203.

XX 05-NOV-1998; 98US-0107219P.

XX (HESK-) HESKA CORP.

XX (NOUN) UNIV NORTHWESTERN.

XX Jardtzy TS, Garman SC, Kinet J;

XX WPI: 2000-365577/31.

XX N-PSDB; AA27302.

XX Three-dimensional model comprising an extracellular domain of a human

XX high affinity Fc epsilon receptor alpha chain protein, useful for

XX identifying inhibitors and useful mutins.

XX Claim 6; Page 462; 463pp; English.

XX The present sequence is the human FcepsilonRIalpha 1-172 protein (also

XX known as PhFcepsilonRIalpha 1-172). Along with either the FcepsilonRI

XX beta and/or gamma subunits, this protein is involved in mast cell

XX activation and the triggering of allergic reactions and anaphylactic

XX shock. The protein can be used to identify useful mutins and inhibitors,

XX which can then be used in the detection of (susceptibility to) allergies

XX and in protecting animals from these allergies

XX Sequence 172 AA;

XX

XX

XX

XX

XX

XX

XX

XX

XX

XX

XX

XX

XX

XX

XX

XX

XX

XX

XX

XX

XX

XX

XX

XX

XX

XX

XX

XX

XX

XX

XX

XX

XX

XX

XX

XX

XX

XX

XX

XX

PN WO200104310-A1.
XX 18-JAN-2001.
XX 13-JUL-2000; 2000WO-US019070.
XX 13-JUL-1999; 99US-0143612P.
PR 02-MAR-2000; 2000US-0186412P.
XX (HESK-) HESKA CORP.
XX (PROM-) PROMEGA CORP.
PA Weber ER, Wood KV, Hall MP;
XX WPI; 2001-103082/11.
XX N-PSDB; AAF24917.
DR A fusion protein, comprising an Fc epsilon receptor domain and a
PT luminescence inducing protein domain that induces a LP substrate to emit
PT light when contacted with the LP domain, useful for detecting
PT immunoglobulin (Ig) E.
XX
XX Claim 16; Page 67; 105pp; English.
XX
XX The present sequence represents a secretable form of a human Fc epsilon
CC receptor (FcepsilonR) alpha-chain. The FcepsilonR protein binds to
CC immunoglobulin (Ig) E. The FcepsilonR domain is used to produce a fusion
CC protein, which also comprises a luminescence inducing protein domain that
CC induces a substrate to emit light when contacted with the luminescence
CC inducing protein domain. The fusion protein may be used to detect IgE. It
CC may also be used to identify a compound capable of inhibiting FcepsilonR
CC protein activity. IgE antibody production is indicative of diseases such
CC as allergies, atopic disease, hyper IgE syndrome, internal parasite
CC infections and B cell neoplasia. Detection of IgE production in an animal
CC following therapy is indicative of the efficacy of the treatment, for
CC example when using treatments intended to disrupt IgE production.
XX
XX Sequence 172 AA;
XX
XX Query Match 100.0%; Score 947; DB 4; Length 172;
XX Best Local Similarity 100.0%; Pred. No. 4.1e-66;
XX Matches 172; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 VPQPKVSLNPPNRRIFKGENVTLTCGNNFFEVSTKWFHNGSLSEETNSLNINAKF 60
DB 1 VPQPKVSLNPPNRRIFKGENVTLTCGNNFFEVSTKWFHNGSLSEETNSLNINAKF 60
QY 61 EDGSEYKCOHQVNESPVYLEVPSDWLLILOASAEVVMGQPLFRLCHGRNWDVYKVIY 120
DB 61 EDGSEYKCOHQVNESPVYLEVPSDWLLILOASAEVVMGQPLFRLCHGRNWDVYKVIY 120
QY 121 YKDGKALKYWNENHISITNATVEDSGTYCTGKVMQLDYSEPLNITVIKA 172
DB 121 YKDGKALKYWNENHISITNATVEDSGTYCTGKVMQLDYSEPLNITVIKA 172
RESULT 4
AA94210
ID AA94210 standard; protein; 176 AA.
XX
XX AA94210;
XX
XX 01-AUG-2000 (first entry)
XX Human PhFcepsilonRIalpha 1-176.
XX Protein co-ordinate data; PhFcepsilonRIalpha 1-176; FcR;
KW FcepsilonRIalpha 1-176; antibody Fc receptor; allergy;
KW anaphylactic shock.
XX Homo sapiens.
XX
XX Key Location/Qualifiers

FT Region
FT /label= Beta_sheet_secondary_structure
FT 14..15
FT /label= beta_sheet_secondary_structure
FT 19..25
FT /label= beta_sheet_secondary_structure
FT 37..40
FT /label= beta_sheet_secondary_structure
FT 44..45
FT /label= beta_sheet_secondary_structure
FT 53..55
FT /label= beta_sheet_secondary_structure
FT 63..68
FT /label= beta_sheet_secondary_structure
FT 76..82
FT /label= beta_sheet_secondary_structure
FT 89..92
FT /label= beta_sheet_secondary_structure
FT 96..97
FT /label= beta_sheet_secondary_structure
FT 101..107
FT /label= beta_sheet_secondary_structure
FT 118..121
FT /label= beta_sheet_secondary_structure
FT 125..127
FT /label= beta_sheet_secondary_structure
FT 135..139
FT /label= beta_sheet_secondary_structure
FT 147..155
FT /label= beta_sheet_secondary_structure
FT 158..170
FT /label= beta_sheet_secondary_structure
XX WO200026246-A2.
XX 11-MAY-2000.
XX 05-NOV-1999; 99WO-US026203.
XX 05-NOV-1998; 98US-0107219P.
XX (HESK-) HESKA CORP.
XX (NOUN) UNIV NORTHWESTERN.
XX Jardtetzky TS, Garman SC, Kinet J;
XX WPI; 2000-365577/31.
XX N-PSDB; AAA27301.
XX Three-dimensional model comprising an extracellular domain of a human
PT high affinity Fc epsilon receptor alpha chain protein, useful for
PT identifying inhibitors and useful muteins.
XX Claim 6; Page 460; 463pp; English.
XX The present sequence is the human FcepsilonRIalpha 1-176 protein (also
CC known as PhFcepsilonRIalpha 1-176). Along with either the FcepsilonRI
CC beta and/or gamma subunits, this protein is involved in mast cell
CC activation and the triggering of allergic reactions and anaphylactic
CC shock. The protein can be used to identify useful muteins and inhibitors,
CC which can then be used in the detection of (susceptibility to) allergies
CC and in protecting animals from these allergies
XX
XX Sequence 176 AA;
XX
XX Query Match 100.0%; Score 947; DB 3; Length 176;
XX Best Local Similarity 100.0%; Pred. No. 4.2e-66;
XX Matches 172; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 VPQPKVSLNPPNRRIFKGENVTLTCGNNFFEVSTKWFHNGSLSEETNSLNINAKF 60
DB 1 VPQPKVSLNPPNRRIFKGENVTLTCGNNFFEVSTKWFHNGSLSEETNSLNINAKF 60

QY 61 EDSEYKCOHQVNESEPVYLEVFSDDLLOASAEVVMGQPLFLRCHGWRNWDVYKVIY 120
 Db 61 EDSEYKCOHQVNESEPVYLEVFSDDLLOASAEVVMGQPLFLRCHGWRNWDVYKVIY 120
 QY 121 YKDGALKYWNHNISITNATVEDSGTYCTGKWQLDYSEPLNITVIKA 172
 Db 121 YKDGALKYWNHNISITNATVEDSGTYCTGKWQLDYSEPLNITVIKA 172

RESULT 5

AA965597
 ID AAG65597 standard; protein; 176 AA.

XX AC AAG65597;

XX DT 07-JAN-2002 (first entry)

XX DE Amino acid sequence of PhCpepsilonRIalpha1-176 protein.

XX KW Antibody receptor protein; FcpepsilonRIalpha protein; immunoglobulin; IgE;
 KW mutein; allergy; protein co-ordinate.

XX OS Homo sapiens.

XX PN WO200169253-A2.

XX PD 20-SEP-2001.

XX PF 14-MAR-2001; 2001WO-US008588.

XX PR 15-MAR-2000; 2000US-0189853P.

XX PA (HESK-) HESKA CORP.

XX PA (NOUN) UNIV NORTHWESTERN.

XX PI Jardtzy TS, Garman SC, Wurzburg BA, Kinet J;

XX DR WPI; 2001-611403/70.

XX DR N-PSDB; AAH47768.

XX PT Three dimensional models of complexes between antibody receptor proteins
 PT and antibodies used to identify modulators of antibody/receptor binding.

XX PS Claim 11; Page 209-210; 213pp; English.

XX CC The invention relates to three dimensional models of complexes between
 CC antibody receptor proteins, especially FcpepsilonRIalpha proteins, and
 CC antibodies, especially Fc-Cep5lon3/Cep5lon4 regions of immunoglobulin
 CC (Ig) E antibodies. The models are used to identify an inhibitor of the
 CC selective binding between a FcpepsilonRIalpha protein and an IgE antibody.
 CC The model identifies crystal contacts between a FcpepsilonRIalpha protein
 CC and an Fc-Cep5lon3/Cep5lon4 region of an IgE antibody. A mutin that
 CC binds to an Fc domain of an antibody (the mutin has improved function
 CC improved stability, increased affinity for an Fc domain of an antibody,
 CC altered substrate specificity, increased affinity for an Fc domain of an
 CC antibody, altered substrate specificity, and increased solubility)
 CC compared to a protein comprising a defined amino acid sequence given in
 CC the specification) is used: to protect an animal from an allergy; detect
 CC an allergy in an animal; and to enhance the performance of an IgE binding
 CC assay. The present sequence represents the amino acid sequence of a
 CC PhCpepsilonRIalpha1-176 protein

XX SQ Sequence 176 AA;

Query Match 100.0%; Score 947; DB 4; Length 176;

Best Local Similarity 100.0%; Pred. No. 4.2e-66;

Matches 172; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 VPQPKVSLNPPNRIKGENVTITCGNNFFVSVSTKWFHNGSLSEETNSSLINIVNAKF 60

Db 1 VPQPKVSLNPPNRIKGENVTITCGNNFFVSVSTKWFHNGSLSEETNSSLINIVNAKF 60

QY 61 EDSEYKCOHQVNESEPVYLEVFSDDLLOASAEVVMGQPLFLRCHGWRNWDVYKVIY 120

Db 61 EDSEYKCOHQVNESEPVYLEVFSDDLLOASAEVVMGQPLFLRCHGWRNWDVYKVIY 120
 QY 121 YKDGALKYWNHNISITNATVEDSGTYCTGKWQLDYSEPLNITVIKA 172
 Db 121 YKDGALKYWNHNISITNATVEDSGTYCTGKWQLDYSEPLNITVIKA 172

RESULT 6

AA96234

ID AAY96234 standard; protein; 182 AA.

XX AC AAY96234;

XX DT 11-SEP-2000 (first entry)

XX DE Recombinant human Fc receptor, FcgammaRIIb, # 4.

XX KW Human; Fc receptor; FcgammaRIIb; immunoglobulin; infection;
 KW immune response; HIV; IgG; immunosuppressive; antirheumatic;
 KW antiinflammatory; AIDS; SLE; multiple myeloma; rheumatoid arthritis;
 KW systemic lupus erythematosus; tumour.

XX OS Homo sapiens.

XX PN EP1006183-A1.

XX PD 07-JUN-2000.

XX PF 03-DEC-1998; 98EP-00122969.

XX PR 03-DEC-1998; 98EP-00122969.

XX PA (PLAC) MAX PLANCK GES FOERDERUNG WISSENSCHAFTEN.

XX DR WPI; 2000-367968/32.

XX DR N-PSDB; AA27472.

XX PT Novel Fc receptor lacking transmembrane domains, a signal peptide, and
 PT glycosylation, useful for diagnosing and treating immune disorders and
 PT cancer.

XX PS Claim 5; Page 15; 60pp; English.

XX CC The present sequence is the recombinant human Fc receptor, FcgammaRIIb.
 CC Fc receptors play an important role in defending the body against
 CC infections. First, pathogens are opsonised by serum immunoglobulins. The
 CC resulting complex then binds to cells expressing Fc receptors. Upon Fc
 CC receptor activation, immune effector pathways are activated, leading to
 CC immune response. The present recombinant Fc receptor consists only of the
 CC extracellular portion of the wildtype receptor and are not glycosylated
 CC i.e. they do not have transmembrane domains or signal peptides. The
 CC recombinant proteins may be used in immunoassays to determine the immune
 CC status of patients with chronic diseases of the immune system, e.g. AIDS,
 CC systemic lupus erythematosus (SLE), multiple myeloma (MM), or rheumatoid
 CC arthritis. In addition, pharmaceutical compositions containing
 CC recombinant proteins may be used to treat or prevent autoimmune diseases,
 CC allergies or tumours, especially AIDS, rheumatoid arthritis or MM. Note:
 CC the present sequence differs from that shown in the sequence listing of
 CC the specification (AAY96232). The AAY96232 sequence has an additional Met
 CC at the N-terminal

XX SQ Sequence 182 AA;

Query Match 100.0%; Score 947; DB 3; Length 182;

Best Local Similarity 100.0%; Pred. No. 4.4e-66;

Matches 172; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 VPQPKVSLNPPNRIKGENVTITCGNNFFVSVSTKWFHNGSLSEETNSSLINIVNAKF 60

Db 2 VPQPKVSLNPPNRIKGENVTITCGNNFFVSVSTKWFHNGSLSEETNSSLINIVNAKF 61

QY 61 EDSEYKCOHQVNESEPVYLEVFSDDLLOASAEVVMGQPLFLRCHGWRNWDVYKVIY 120

Db 62 EDSEYKQHQVNESEPVYLEVFSWLLQLQASAEVVMGQPLFLRCHGWRNDVYKVIY 121
QY 121 YKDGALKYWEHNHNSITNATVEDSGTYCTGKWQWLDYSEPLNITVIKA 172
Db 122 YKDGALKYWEHNHNSITNATVEDSGTYCTGKWQWLDYSEPLNITVIKA 173

RESULT 7
AAY96232
ID AAY96232 standard; protein; 183 AA.
XX
AC AAY96232;
XX
DT 11-SEP-2000 (first entry)
XX
DE Recombinant human Fc receptor, Fc gammaRIIb, # 2.
XX Human; Fc receptor; Fc gammaRIIb; immunoglobulin; infection;
KW immune response; HIV; IGG; immunosuppressive; antirheumatic;
KW antiinflammatory; AIDS; SLE; multiple myeloma; rheumatoid arthritis;
XX systemic lupus erythematosus; tumour.
XX
OS Homo sapiens.
XX
PN EP1006183-A1.
XX
PD 07-JUN-2000.
XX
PF 03-DEC-1998; 98BP-00122969.
XX
PR 03-DEC-1998; 98EP-00122969.
XX
XX (PLAC) MAX PLANCK GES FOERDERUNG WISSENSCHAFTEN.
PA
XX WPI; 2000-367968/32.
DR N-PSDB; AAA27472.
XX

Novel Fc receptor lacking transmembrane domains, a signal peptide, and glycosylation, useful for diagnosing and treating immune disorders and cancer.
Claim 5; Page 45-46; 60pp; English.
XX
The present sequence is the recombinant human Fc receptor, Fc gammaRIIb. Fc receptors play an important role in defending the body against infections. First, pathogens are opsonised by serum immunoglobulins. The resulting complex then binds to cells expressing Fc receptors. Upon Fc receptor activation, immune effector pathways are activated, leading to immune response. The present recombinant Fc receptor consists only of the extracellular portion of the wildtype receptor and are not glycosylated i.e. they do not have transmembrane domains or signal peptides. The recombinant proteins may be used in immunoassays to determine the immune status of patients with chronic diseases of the immune system, e.g. AIDS, systemic lupus erythematosus (SLE), multiple myeloma (MM), or rheumatoid arthritis. In addition, pharmaceutical compositions containing recombinant proteins may be used to treat or prevent autoimmune diseases, allergies or tumours, especially AIDS, rheumatoid arthritis or MM. Note: the present sequence differs from that shown on Page 15 of the specification (AAY96234). The present sequence has an additional Met at the N-terminal
XX
SQ Sequence 183 AA;

Query Match 100.0%; Score 947; DB 3; Length 183;
Best Local Similarity 100.0%; Pred. No. 4.4e-66;
Matches 172; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 VPQPKVSLNPPWNRIFKGENVTLTCGNPFVSVSTKWFHNGSLSEETNSSLNIVNAKF 60
Db 3 VPQPKVSLNPPWNRIFKGENVTLTCGNPFVSVSTKWFHNGSLSEETNSSLNIVNAKF 62
QY 61 EDSEYKQHQVNESEPVYLEVFSWLLQLQASAEVVMGQPLFLRCHGWRNDVYKVIY 120

Db 63 EDSEYKQHQVNESEPVYLEVFSWLLQLQASAEVVMGQPLFLRCHGWRNDVYKVIY 122
QY 121 YKDGALKYWEHNHNSITNATVEDSGTYCTGKWQWLDYSEPLNITVIKA 172
Db 123 YKDGALKYWEHNHNSITNATVEDSGTYCTGKWQWLDYSEPLNITVIKA 174

RESULT 8
AAR45778
ID AAR45778 standard; protein; 197 AA.
XX
AC AAR45778;
XX
DT 25-MAR-2003 (revised)
DT 12-SEP-1994 (first entry)
XX
DE Human dihydrofolate reductase (DHFR).
XX Dihydrofolate reductase; DHFR; marker; transformation.
KW
OS Homo sapiens.
XX
PN WO9403598-A1.
XX
PD 17-FEB-1994.
XX
PF 03-AUG-1993; 93WO-JP001085.
XX
PR 04-AUG-1992; 92JP-00229227.
PR 10-AUG-1992; 92JP-00213002.
PR 08-OCT-1992; 92JP-00270513.
PR 08-OCT-1992; 92JP-00270514.
PR 08-OCT-1992; 92JP-00270515.
XX
PA (GREC) GREEN CROSS CORP.
XX
PI Ra C, Naito K, Hiram M, Okumura K;
XX
DR WPI; 1994-065687/08.
DR N-PSDB; AAR455969.
XX

Antiallergic peptide derived from high-affinity immunoglobulin E receptor - binds to human immunoglobulin E to block allergic reactions at source.
Disclosure; Page 24-25; 37pp; Japanese.
XX
The dihydrofolate reductase (DHFR) gene was used in the construction of a vector as a selectable marker. The resulting vector was used to transform DHFR-deficient CHO cells. (Updated on 25-MAR-2003 to correct PN field.)
XX
SQ Sequence 197 AA;
Query Match 100.0%; Score 947; DB 2; Length 197;
Best Local Similarity 100.0%; Pred. No. 4.8e-66;
Matches 172; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 VPQPKVSLNPPWNRIFKGENVTLTCGNPFVSVSTKWFHNGSLSEETNSSLNIVNAKF 60
Db 26 VPQPKVSLNPPWNRIFKGENVTLTCGNPFVSVSTKWFHNGSLSEETNSSLNIVNAKF 85
QY 61 EDSEYKQHQVNESEPVYLEVFSWLLQLQASAEVVMGQPLFLRCHGWRNDVYKVIY 120
Db 86 EDSEYKQHQVNESEPVYLEVFSWLLQLQASAEVVMGQPLFLRCHGWRNDVYKVIY 145

Query Match 100.0%; Score 947; DB 3; Length 183;
Best Local Similarity 100.0%; Pred. No. 4.4e-66;
Matches 172; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 VPQPKVSLNPPWNRIFKGENVTLTCGNPFVSVSTKWFHNGSLSEETNSSLNIVNAKF 60
Db 3 VPQPKVSLNPPWNRIFKGENVTLTCGNPFVSVSTKWFHNGSLSEETNSSLNIVNAKF 62
QY 61 EDSEYKQHQVNESEPVYLEVFSWLLQLQASAEVVMGQPLFLRCHGWRNDVYKVIY 120

```

XX AAB31585;
AC
XX 30-APR-2001 (first entry)
XX
DE A Fc epsilon receptor alpha-chain extracellular domain.
XX
XX Fc epsilon receptor; FcepsilonR; immunoglobulin E; IgE; atopic disease;
XX luminescence inducing protein; allergy; hyper IgE syndrome;
XX internal parasite infection; B cell neoplasia.
XX
OS Homo sapiens.
XX
XX WO200104310-A1.
XX
XX 18-JAN-2001.
XX
XX 13-JUL-2000; 2000WO-US019070.
XX
XX 13-JUL-1999; 99US-0143612P.
XX 02-MAR-2000; 2000US-0186412P.
XX
XX (HESK-) HESKA CORP.
XX (PROM-) PROMEGA CORP.
XX
XX Weber ER, Wood KV, Hall MP;
XX
XX WPI: 2001-103082/11.
XX N-PSDB; AAF24915.
XX
XX A fusion protein, comprising an Fc epsilon receptor domain and a
XX luminescence inducing protein domain that induces a LP substrate to emit
XX light when contacted with the LP domain, useful for detecting
XX immunoglobulin (Ig) E.
XX
XX Claim 16; Page 65; 105pp; English.
XX
XX The present sequence represents the extracellular domain of a human Fc
XX epsilon receptor (FcepsilonR) alpha-chain. The FcepsilonR protein binds
XX to immunoglobulin (Ig) E. The FcepsilonR domain is used to produce a
XX fusion protein, which also comprises a luminescence inducing protein
XX domain that induces a substrate to emit light when contacted with the
XX luminescence inducing protein domain. The fusion protein may be used to
XX detect IgE. It may also be used to identify a compound capable of
XX inhibiting FcepsilonR protein activity. IgE antibody production is
XX indicative of diseases such as allergies, atopic disease, hyper IgE
XX syndrome, internal parasite infections and B cell neoplasia. Detection of
XX IgE production in an animal following therapy is indicative of the
XX efficacy of the treatment, for example when using treatments intended to
XX disrupt IgE production
XX
XX Sequence 197 AA;
XX
Query Match 100.0%; Score 947; DB 4; Length 197;
Best Local Similarity 100.0%; Pred. No. 4.8e-66;
Matches 172; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 VPQPKVSLNPPWNRIFKGENVTITCGNNPFVSVSTKWFHNGSLSEETNSSLNINAKF 60
Db 26 VPQPKVSLNPPWNRIFKGENVTITCGNNPFVSVSTKWFHNGSLSEETNSSLNINAKF 65
QY 61 EDSEYKCOHQOVNESEPVYLEVFSDWLLLOQSAEVVMGQPLFLRCHGRNWDVYKVIY 120
Db 86 EDSEYKCOHQOVNESEPVYLEVFSDWLLLOQSAEVVMGQPLFLRCHGRNWDVYKVIY 145
QY 121 YKGEALKYWEHNHISITNATVEDSGTYCTGKWQLDYSEPLNITVIKA 172
Db 146 YKGEALKYWEHNHISITNATVEDSGTYCTGKWQLDYSEPLNITVIKA 197

```

RESULT 10
AAB31585
ID AAB31585 standard; protein; 232 AA.

```

XX AAB31585;
AC
XX 30-APR-2001 (first entry)
XX
DE Amino acid sequence of Fc epsilon receptor alpha-chain mature protein.
XX
XX Fc epsilon receptor; FcepsilonR; immunoglobulin E; IgE; atopic disease;
XX luminescence inducing protein; allergy; hyper IgE syndrome;
XX internal parasite infection; B cell neoplasia.
XX
OS Homo sapiens.
XX
XX WO200104310-A1.
XX
XX 18-JAN-2001.
XX
XX 13-JUL-2000; 2000WO-US019070.
XX
XX 13-JUL-1999; 99US-0143612P.
XX 02-MAR-2000; 2000US-0186412P.
XX
XX (HESK-) HESKA CORP.
XX (PROM-) PROMEGA CORP.
XX
XX Weber ER, Wood KV, Hall MP;
XX
XX WPI: 2001-103082/11.
XX N-PSDB; AAF24913.
XX
XX A fusion protein, comprising an Fc epsilon receptor domain and a
XX luminescence inducing protein domain that induces a LP substrate to emit
XX light when contacted with the LP domain, useful for detecting
XX immunoglobulin (Ig) E.
XX
XX Claim 16; Page 62-63; 105pp; English.
XX
XX The present sequence represents a human Fc epsilon receptor (FcepsilonR)
XX alpha-chain mature protein, that binds to immunoglobulin (Ig) E. The
XX FcepsilonR domain is used to produce a fusion protein, which also
XX comprises a luminescence inducing protein domain that induces a substrate
XX to emit light when contacted with the luminescence inducing protein
XX domain. The fusion protein may be used to detect IgE. It may also be used
XX to identify a compound capable of inhibiting FcepsilonR protein activity.
XX IgE antibody production is indicative of diseases such as allergies,
XX atopic disease, hyper IgE syndrome, internal parasite infections and B
XX cell neoplasia. Detection of IgE production in an animal following
XX therapy is indicative of the efficacy of the treatment, for example when
XX using treatments intended to disrupt IgE production
XX
XX Sequence 232 AA;
XX
Query Match 100.0%; Score 947; DB 4; Length 232;
Best Local Similarity 100.0%; Pred. No. 5.8e-66;
Matches 172; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 VPQPKVSLNPPWNRIFKGENVTITCGNNPFVSVSTKWFHNGSLSEETNSSLNINAKF 60
Db 1 VPQPKVSLNPPWNRIFKGENVTITCGNNPFVSVSTKWFHNGSLSEETNSSLNINAKF 60
QY 61 EDSEYKCOHQOVNESEPVYLEVFSDWLLLOQSAEVVMGQPLFLRCHGRNWDVYKVIY 120
Db 61 EDSEYKCOHQOVNESEPVYLEVFSDWLLLOQSAEVVMGQPLFLRCHGRNWDVYKVIY 120
QY 121 YKGEALKYWEHNHISITNATVEDSGTYCTGKWQLDYSEPLNITVIKA 172
Db 121 YKGEALKYWEHNHISITNATVEDSGTYCTGKWQLDYSEPLNITVIKA 172

```

RESULT 11
AAR26064
ID AAR26064 standard; protein; 235 AA.
XX

AC AAR26064;
 XX 25-MAR-2003 (revised)
 DT 02-FEB-1993 (first entry)
 XX Human FCERI alpha-subunit and IL-2 hybrid protein.
 XX High affinity Fc immunoglobulin E receptor; IGE; antibody; interleukin-2;
 KW histamine release; allergy.
 XX Homo sapiens.
 OS
 XX Key Location/Qualifiers
 FH 26..201
 FT /label= human_FcERI_alpha-subunit
 FT /note= "epitope recognised by new MAB"
 XX
 XX EP499112-A1.
 XX 19-AUG-1992.
 XX 03-FEB-1992; 92EP-00101732.
 XX 11-FEB-1991; 91US-00653936.
 XX (HOFF) HOFFMANN LA ROCHE & CO AG F.
 XX Chizzonite RA, Hakimi J, Kochan JP;
 XX WPI; 1992-277871/34.
 XX Monoclonal antibodies bind to alpha sub-unit of Fc IGE receptor - for
 PT treatment and prevention of IGE induced allergic diseases, also for
 PT measuring alpha sub-unit and IGE levels in biological fluids.
 XX Disclosure; Page 8; 30pp; English.
 XX This is a preferred protein for use in generating the monoclonal
 CC antibodies of the invention. The protein comprises an epitope of the
 CC human FCERI alpha-subunit to which the cytoplasmic and transmembrane
 CC regions of the IL-2 receptor have been fused. (Cytoplasmic and
 CC transmembrane regions from receptors other IL-2 receptor can be also
 CC used). The specification includes a nucleotide coding sequence which is a
 CC preferred fusion gene (see AAR2767); the polypeptide which is decoded
 CC from that fusion gene differs from the amino acid sequence AAR26064 as
 CC follows: amino acids 5-7 are Arg-Ile-Leu (not Met-Glu-Ser), amino acid
 CC 209 is Cys (not Lys), amino acid 229 is Ser (not Arg), Arg233 is absent
 CC and an additional C-terminal amino acid (Phe) is present. (Updated on 25-
 CC MAR-2003 to correct PN field.)
 XX
 SQ Sequence 235 AA;
 Query Match 100.0%; Score 947; DB 2; Length 235;
 Best Local Similarity 100.0%; Pred. No. 5.9e-66;
 Matches 172; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 VPQKPKVSLNPPWNRIFKGENVTLTCNGNNFFVSSSTKWFHNGSLSEETNSSLNIVNAKF 60
 DB 26 VPQKPKVSLNPPWNRIFKGENVTLTCNGNNFFVSSSTKWFHNGSLSEETNSSLNIVNAKF 85
 QY 61 EDGSEYKCOHQOVNESEPVYLEVFSDWLLQLQASAEVVMGQPLFLRCHGWRNWDVYKVIY 120
 DB 86 EDGSEYKCOHQOVNESEPVYLEVFSDWLLQLQASAEVVMGQPLFLRCHGWRNWDVYKVIY 145
 QY 121 YKDGALKYWEYENHNISITNATVEDSGTYCTGKWQLDYSEPLNITVIKA 172
 DB 146 YKDGALKYWEYENHNISITNATVEDSGTYCTGKWQLDYSEPLNITVIKA 197
 RESULT 12
 AAP90385
 ID AAP90385 standard; protein; 257 AA.
 XX

AC AAP90385;
 XX 24-OCT-2003 (revised)
 DT 25-MAR-2003 (revised)
 DT 01-NOV-1989 (first entry)
 XX Alpha subunit of human mast cell IGE surface receptor.
 XX Immunoglobulin E receptor alpha subunit; allergies;
 KW non-peptide drug design; human.
 XX Homo sapiens; (Human); mast cell line.
 OS KU812.
 XX W08905352-A.
 XX 15-JUN-1989.
 XX 29-NOV-1988; 88WO-US004255.
 XX 01-DEC-1987; 87US-00127214.
 XX (HARD) HARVARD COLLEGE.
 XX (USSH) NAT INST OF HEALTH.
 XX Leder P, Benfey P;
 XX WPI; 1989-192698/26.
 XX N-PSDB; AAN90126.
 XX CDNA encoding IGE receptor alpha-sub-unit - used to treat allergies.
 PT Disclosure; Fig 4; 17pp; English.
 XX Immunoglobulin E receptor alpha subunit of human mast cell IGE surface
 CC receptor (see corresp. AAN90126). Used to produce antibodies which can
 CC diagnose IGE receptor levels, measure and treat allergies, and design non
 CC -peptide drugs. (Updated on 25-MAR-2003 to correct PA field.) (Updated on
 CC 24-OCT-2003 to standardise OS field)
 XX
 SQ Sequence 257 AA;
 Query Match 100.0%; Score 947; DB 1; Length 257;
 Best Local Similarity 100.0%; Pred. No. 6.5e-66;
 Matches 172; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 VPQKPKVSLNPPWNRIFKGENVTLTCNGNNFFVSSSTKWFHNGSLSEETNSSLNIVNAKF 60
 DB 26 VPQKPKVSLNPPWNRIFKGENVTLTCNGNNFFVSSSTKWFHNGSLSEETNSSLNIVNAKF 85
 QY 61 EDGSEYKCOHQOVNESEPVYLEVFSDWLLQLQASAEVVMGQPLFLRCHGWRNWDVYKVIY 120
 DB 86 EDGSEYKCOHQOVNESEPVYLEVFSDWLLQLQASAEVVMGQPLFLRCHGWRNWDVYKVIY 145
 QY 121 YKDGALKYWEYENHNISITNATVEDSGTYCTGKWQLDYSEPLNITVIKA 172
 DB 146 YKDGALKYWEYENHNISITNATVEDSGTYCTGKWQLDYSEPLNITVIKA 197
 RESULT 13
 AAR05025
 ID AAR05025 standard; protein; 257 AA.
 XX
 XX AAR05025;
 XX 02-OCT-1990 (first entry)
 XX Alpha subunit of human high affinity IGE receptor.
 DE high affinity IGE receptor; alpha subunit of IGE receptor; human;
 KW allergic response; ss.
 XX
 OS Synthetic.

```

XX WO9004640-A.
XX PN
XX PD
XX 03-MAY-1990.
XX PF
XX 18-OCT-1988; 88US-00259065.
XX PR
XX 18-OCT-1988; 88US-00259065.
XX PA
XX (USDC ) US SEC OF COMMERCE.
XX PI
XX Kinet JP, Metzger H;
XX WPI; 1990-164023/21.
XX DR
XX N-PSDB; AAQ04644.
XX PT
XX DNA sequences for sub-unit peptide(s) of high affinity IgE receptor - and
XX derived polypeptides, for therapy and diagnosis of allergies, and studies
XX of IgE receptor interaction.
XX PS
XX Disclosure; Page ?; -pp; English.
XX CC
XX The high affinity receptor is a tetrameric complex consisting of 2 gamma
XX subunits and one each of subunits alpha and beta. It is expressed on mast
XX cells and is involved in the allergic response. COS-7 cells cotransfected
XX with cDNA for all 3 intact subunit types (derived from rat basophilic
XX leukaemia cells) express receptor on their surfaces. Detailed study of
XX the receptors is now possible. See also AAQ04643 and AAQ04645-6
XX SQ
XX Sequence 257 AA;
XX
XX Query Match 100.0%; Score 947; DB 2; Length 257;
XX Best Local Similarity 100.0%; Pred. No. 6.5e-66;
XX Matches 172; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
XX QY 1 VPQPKVSLNPPWNRIFKGENVTILTCGNPFVSVSTKWFHNGSLSEETNSLNIIVNAKF 60
XX DB 26 VPQPKVSLNPPWNRIFKGENVTILTCGNPFVSVSTKWFHNGSLSEETNSLNIIVNAKF 85
XX
XX QY 61 EDSGEYKQHQOVNESEPVYLEVFSDWLLQLQASAEVVMGQPLFLRCHGWRNWDVYKVIY 120
XX DB 86 EDSGEYKQHQOVNESEPVYLEVFSDWLLQLQASAEVVMGQPLFLRCHGWRNWDVYKVIY 145
XX
XX QY 121 YKDGELKXYWYENHNISITNATVEDSGTYCTGKWOLDYSEPLNITVIKA 172
XX DB 146 YKDGELKXYWYENHNISITNATVEDSGTYCTGKWOLDYSEPLNITVIKA 197
XX
XX RESULT 14
XX AAR14772
XX ID AAR14772 standard; protein; 257 AA.
XX XX
XX AC AAR14772;
XX XX
XX 25-MAR-2003 (revised)
XX DT 17-DEC-2001 (revised)
XX DT 03-FEB-1992 (first entry)
XX XX
XX DE Human Fc(epsilon)RI alpha subunit.
XX XX
XX Immunoglobulin; receptor; high affinity receptor.
XX KW
XX Homo sapiens.
XX OS
XX
XX Key Location/Qualifiers
XX Peptide 1..25
XX FT /label= signal
XX FT 26..257
XX FT /label= alpha_subunit
XX FT 80..104
XX FT /label= homologous_domain
XX FT /notes= "homologous to residues 163-190"
XX FT 163..190

```

```

FT FT /label= homologous_domain
FT FT /notes= "homologous to residues 80-104"
FT FT 205..224
FT FT /label= transmembrane
FT FT 225..257
FT FT /label= cytoplasmic
XX XX
XX USN7626704-N.
XX PN
XX 15-OCT-1991.
XX XX
XX 14-DEC-1990; 90US-00626704.
XX PF
XX 14-DEC-1990; 90US-00626704.
XX PR
XX (USSH ) NAT INST OF HEALTH.
XX PA
XX Kinet JP, Metzger H;
XX PI
XX WPI; 1991-346755/47.
XX DR
XX N-PSDB; AAQ14736.
XX DR
XX DNA coding alpha, beta and gamma-units of ige high affinity receptor -
XX PT are used to prepare recombinant polypeptide(s) for treating allergy, drug
XX screening or monitoring IGE level.
XX PT
XX Disclosure; Fig 1; 58pp; English.
XX PS
XX A lambda gtl1 library was prepared from poly-A RNA isolated from KUB12
XX CC cells. Screening was by a cDNA fragment from the rat Fc(epsilon)RI alpha
XX CC cDNA corresponding to nucleotides 119-781. Positive clones were subcloned
XX CC and sequenced. This amino acid sequence was deduced from the cDNA clone.
XX CC (Note: Revised entry submitted to correct the patent number format of US
XX CC Government-owned NTIS applications to prevent clashes with ongoing US
XX CC granted patent numbers. For further information please visit the Derwent
XX CC web site at www.derwent.com/dwpi/updates/ntis_us.html.) (Updated on 25-
XX CC MAR-2003 to correct PF field.)
XX SQ
XX Sequence 257 AA;
XX
XX Query Match 100.0%; Score 947; DB 2; Length 257;
XX Best Local Similarity 100.0%; Pred. No. 6.5e-66;
XX Matches 172; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
XX QY 1 VPQPKVSLNPPWNRIFKGENVTILTCGNPFVSVSTKWFHNGSLSEETNSLNIIVNAKF 60
XX DB 26 VPQPKVSLNPPWNRIFKGENVTILTCGNPFVSVSTKWFHNGSLSEETNSLNIIVNAKF 85
XX
XX QY 61 EDSGEYKQHQOVNESEPVYLEVFSDWLLQLQASAEVVMGQPLFLRCHGWRNWDVYKVIY 120
XX DB 86 EDSGEYKQHQOVNESEPVYLEVFSDWLLQLQASAEVVMGQPLFLRCHGWRNWDVYKVIY 145
XX
XX QY 121 YKDGELKXYWYENHNISITNATVEDSGTYCTGKWOLDYSEPLNITVIKA 172
XX DB 146 YKDGELKXYWYENHNISITNATVEDSGTYCTGKWOLDYSEPLNITVIKA 197
XX
XX RESULT 15
XX AAR42336
XX ID AAR42336 standard; protein; 257 AA.
XX XX
XX AC AAR42336;
XX XX
XX 25-MAR-2003 (revised)
XX DT 21-JUN-1994 (first entry)
XX DT
XX Human FcεRI alpha.
XX DE
XX IGE; immunoglobulin E receptor; beta subunit; basophil; allergy;
XX KW aggregation; signal transduction; diagnosis; antagonist.
XX KW
XX Homo sapiens.
XX OS
XX

```

	Query Match	100.0%	Score 947;	DB 2;	Length 257;
	Best Local Similarity	100.0%;	Pred. No. 6.5e-66;		
	Matches 172;	Conservative 0;	Mismatches 0;	Indels 0;	Gaps 0;
Qy	1	VPOKPKVSLNPWNRIKGENVTITCTGNNFFVSVSTKWFHNGSLSEETSSSLINLVNAKF	60		
Db	26	VPOKPKVSLNPWNRIKGENVTITCTGNNFFVSVSTKWFHNGSLSEETSSSLINLVNAKF	85		
Qy	61	EDSGEYKQCHQOVNESEPVYLEVFSDDLQLQASAEVVMGQPLFLRCHGWRNDVYKVIY	120		
Db	86	EDSGEYKQCHQOVNESEPVYLEVFSDDLQLQASAEVVMGQPLFLRCHGWRNDVYKVIY	145		
Qy	121	YDGGALKYWNHNISITNATVDSGTYYCTGKWQOLDYSEPLNITVKA	172		
Db	146	YDGGALKYWNHNISITNATVDSGTYYCTGKWQOLDYSEPLNITVKA	197		

Search completed: October 6, 2004, 09:03:08
Job time : 39.8904 secs

This Page Blank (uspto)

GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.

OM protein - protein search, using sw model

Run on: October 6, 2004, 08:59:40 ; Search time 11.2261 Seconds
(without alignments)
790.984 Million cell updates/sec

Title: US-10-763-400-13

Perfect score: 947

Sequence: 1 VPQPKVSLNPPWNRIFKGE.....GKWLQDYSEPLNITVIKA 172

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 389414 seqs, 51625971 residues

Total number of hits satisfying chosen parameters: 389414

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

Issued Patents AA.*
1: /cgn2_6/ptodata/2/iaa/5A_COMB.pep.*
2: /cgn2_6/ptodata/2/iaa/5B_COMB.pep.*
3: /cgn2_6/ptodata/2/iaa/6A_COMB.pep.*
4: /cgn2_6/ptodata/2/iaa/6B_COMB.pep.*
5: /cgn2_6/ptodata/2/iaa/PCFUS_COMB.pep.*
6: /cgn2_6/ptodata/2/iaa/backfiles1.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	947	100.0	172	2	US-08-756-387B-13
2	947	100.0	172	4	US-09-285-873-13
3	947	100.0	172	4	US-09-245-764-9
4	947	100.0	172	4	US-09-944-277A-13
5	947	100.0	197	2	US-08-756-387B-11
6	947	100.0	197	4	US-09-285-873-11
7	947	100.0	197	4	US-09-944-277A-11
8	947	100.0	232	1	US-07-869-933-13
9	947	100.0	232	2	US-08-756-387B-6
10	947	100.0	232	3	US-09-103-663-13
11	947	100.0	232	4	US-09-285-873-6
12	947	100.0	232	4	US-09-944-277A-6
13	947	100.0	257	1	US-07-869-933-11
14	947	100.0	257	2	US-08-756-387B-2
15	947	100.0	257	3	US-09-103-663-11
16	947	100.0	257	4	US-09-285-873-2
17	947	100.0	257	4	US-08-897-956A-1
18	947	100.0	257	4	US-09-944-277A-2
19	947	100.0	978	4	US-08-897-956A-3
20	941	99.4	197	3	US-08-788-954-2
21	931	98.3	193	5	US-08-765-536-1
22	931	98.3	193	5	PCT-US95-08401-1
23	570	60.2	201	3	US-09-015-734-12
24	570	60.2	201	4	US-09-515-311-12
25	570	60.2	236	3	US-09-015-734-7
26	570	60.2	236	4	US-09-515-311-7
27	570	60.2	255	3	US-09-015-734-2

Sequence 2, Appli
Sequence 14, Appl
Sequence 31, Appl
Sequence 4, Appl
Sequence 28, Appl
Sequence 24, Appl
Sequence 20, Appl
Sequence 9, Appl
Sequence 9, Appl
Sequence 10, Appl
Sequence 13, Appl
Sequence 13, Appl
Sequence 12, Appl
Sequence 12, Appl
Sequence 12, Appl
Sequence 7, Appl
Sequence 7, Appl

ALIGNMENTS

RESULT 1
US-08-756-387B-13
; Sequence 13, Application US/08756387B
; Patent No. 5943294
; GENERAL INFORMATION:
; APPLICANT: Frank, Glenn R.
; APPLICANT: Porter, James P.
; APPLICANT: Rushlow, Keith E.
; APPLICANT: Wassom, Donald L.
; TITLE OF INVENTION: Method to Detect Ige
; NUMBER OF SEQUENCES: 13
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Carol Talkington Verser, Ph.D.
; ADDRESS: Heska Corporation
; STREET: 1825 Sharp Point Drive
; CITY: Fort Collins
; STATE: Colorado
; COUNTRY: USA
; ZIP: 80525
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: Windows 95
; SOFTWARE: WordPerfect for Windows, Version 7.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/756,387B
; FILING DATE: No. 5945294ember 26, 1996
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Verser, Carol Talkington
; REGISTRATION NUMBER: 37,459
; REFERENCE/DOCKET NUMBER: DI-1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 970/493-7272
; TELEFAX: 970/484-9505
; INFORMATION FOR SEQ ID NO: 13:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 172 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-756-387B-13

Query Match 100.0%; Score 947; DB 2; Length 172;
Best Local Similarity 100.0%; Pred. No. 3e-86;
Matches 172; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 VPQPKVSLNPPWNRIFKGENVLTTCGNPFVSVSTKXTHNGSLSEETNSSLNINAKF 60
Db 1 VPQPKVSLNPPWNRIFKGENVLTTCGNPFVSVSTKXTHNGSLSEETNSSLNINAKF 60

QY 61 EDSEYKCHQVNESEPVYLFVSDWLLLOQSAEVMGQPLFLRCHGRWWDVYKVIY 120
 Db 61 EDSEYKCHQVNESEPVYLFVSDWLLLOQSAEVMGQPLFLRCHGRWWDVYKVIY 120
 QY 121 YKDGEALKYWNHNISITNATVEDSGTYCTGKWQLDYSEPLNITVIKA 172
 Db 121 YKDGEALKYWNHNISITNATVEDSGTYCTGKWQLDYSEPLNITVIKA 172

RESULT 2

US-09-285-873-13
 ; Sequence 13, Application US/09285873
 ; Patent No. 6309832
 ; GENERAL INFORMATION:
 ; APPLICANT: Frank, Glenn R.
 ; APPLICANT: Porter, James P.
 ; APPLICANT: Rushlow, Keith E.
 ; APPLICANT: Wassom, Donald L.
 ; TITLE OF INVENTION: Method to Detect Ige
 ; NUMBER OF SEQUENCES: 13
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: Carol Talkington Verser, Ph.D.
 ; ADDRESSEE: Heska Corporation
 ; STREET: 1825 Sharp Point Drive
 ; CITY: Fort Collins
 ; STATE: Colorado
 ; COUNTRY: USA
 ; ZIP: 80525
 ; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: Floppy disk
 ; COMPUTER: IBM PC compatible
 ; OPERATING SYSTEM: Windows 95
 ; SOFTWARE: Wordperfect for Windows, Version 7.0
 ; CURRENT APPLICATION DATA:
 ; APPLICATION NUMBER: US/09/285,873
 ; FILING DATE:
 ; CLASSIFICATION:
 ; PRIOR APPLICATION DATA:
 ; APPLICATION NUMBER: US/08/756,387
 ; FILING DATE: No. 6309832ember 26, 1996
 ; ATTORNEY/AGENT INFORMATION:
 ; NAME: Verser, Carol Talkington
 ; REGISTRATION NUMBER: 37,459
 ; REFERENCE/DOCKET NUMBER: DI-1
 ; TELECOMMUNICATION INFORMATION:
 ; TELEPHONE: 970/493-7272
 ; TELEFAX: 970/484-9505
 ; INFORMATION FOR SEQ ID NO: 13:
 ; SEQUENCE CHARACTERISTICS:
 ; LENGTH: 172 amino acids
 ; TYPE: amino acid
 ; TOPOLOGY: linear
 ; MOLECULE TYPE: protein
 ; US-09-285-873-13

Query Match 100.0%; Score 947; DB 4; Length 172;
 Best Local Similarity 100.0%; Pred. No. 3e-86;
 Matches 172; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 VPQKPKVSLNPPNRIKGENVTLCNGNNFEVSTKWFHNGSLSEETNSLNIIVNAKF 60
 Db 1 VPQKPKVSLNPPNRIKGENVTLCNGNNFEVSTKWFHNGSLSEETNSLNIIVNAKF 60
 QY 61 EDSEYKCHQVNESEPVYLFVSDWLLLOQSAEVMGQPLFLRCHGRWWDVYKVIY 120
 Db 61 EDSEYKCHQVNESEPVYLFVSDWLLLOQSAEVMGQPLFLRCHGRWWDVYKVIY 120
 QY 121 YKDGEALKYWNHNISITNATVEDSGTYCTGKWQLDYSEPLNITVIKA 172
 Db 121 YKDGEALKYWNHNISITNATVEDSGTYCTGKWQLDYSEPLNITVIKA 172

RESULT 3

US-09-245-764-9
 ; Sequence 9, Application US/09245764
 ; Patent No. 6675105
 ; GENERAL INFORMATION:
 ; APPLICANT: Hogarth, P. Mark
 ; APPLICANT: Powell, Maree S.
 ; APPLICANT: McKenzie, Ian P.C.
 ; APPLICANT: Maxwell, Kelly F.
 ; APPLICANT: Garrett, Thomas P.J.
 ; APPLICANT: Epa, Vidana
 ; TITLE OF INVENTION: THREE DIMENSIONAL STRUCTURES AND MODELS OF FC RECEPTORS
 ; FILE REFERENCE: 4102-4
 ; CURRENT APPLICATION NUMBER: US/09/245,764
 ; CURRENT FILING DATE: 1999-02-05
 ; EARLIER APPLICATION NUMBER: 60/099,994
 ; EARLIER FILING DATE: 1998-09-11
 ; EARLIER APPLICATION NUMBER: 60/073,972
 ; EARLIER FILING DATE: 1998-02-06
 ; NUMBER OF SEQ ID NOS: 15
 ; SOFTWARE: PatentIn Ver. 2.0
 ; SEQ ID NO 9
 ; LENGTH: 172
 ; TYPE: PRT
 ; ORGANISM: Homo sapiens
 ; US-09-245-764-9

Query Match 100.0%; Score 947; DB 4; Length 172;
 Best Local Similarity 100.0%; Pred. No. 3e-86;
 Matches 172; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 VPQKPKVSLNPPNRIKGENVTLCNGNNFEVSTKWFHNGSLSEETNSLNIIVNAKF 60
 Db 1 VPQKPKVSLNPPNRIKGENVTLCNGNNFEVSTKWFHNGSLSEETNSLNIIVNAKF 60
 QY 61 EDSEYKCHQVNESEPVYLFVSDWLLLOQSAEVMGQPLFLRCHGRWWDVYKVIY 120
 Db 61 EDSEYKCHQVNESEPVYLFVSDWLLLOQSAEVMGQPLFLRCHGRWWDVYKVIY 120
 QY 121 YKDGEALKYWNHNISITNATVEDSGTYCTGKWQLDYSEPLNITVIKA 172
 Db 121 YKDGEALKYWNHNISITNATVEDSGTYCTGKWQLDYSEPLNITVIKA 172

RESULT 4

US-09-944-277A-13
 ; Sequence 13, Application US/09944277A
 ; Patent No. 6682894
 ; GENERAL INFORMATION:
 ; APPLICANT: Frank, Glenn R.
 ; Porter, James P.
 ; Rushlow, Keith E.
 ; Wassom, Donald L.
 ; TITLE OF INVENTION: Method to Detect Ige
 ; NUMBER OF SEQUENCES: 13
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: Carol Talkington Verser, Ph.D.
 ; ADDRESSEE: Heska Corporation
 ; STREET: 1825 Sharp Point Drive
 ; CITY: Fort Collins
 ; STATE: Colorado
 ; COUNTRY: USA
 ; ZIP: 80525
 ; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: Floppy disk
 ; COMPUTER: IBM PC compatible
 ; OPERATING SYSTEM: Windows 95
 ; SOFTWARE: Wordperfect for Windows, Version 7.0
 ; CURRENT APPLICATION DATA:
 ; APPLICATION NUMBER: US/09/944,277A
 ; FILING DATE: 30-Aug-2001
 ; CLASSIFICATION: <Unknown>

;; PRIOR APPLICATION DATA:
;; APPLICATION NUMBER: 09/285,873
;; FILING DATE: 1999-03-31
;; ATTORNEY/AGENT INFORMATION:
;; NAME: Verser, Carol Talkington
;; REGISTRATION NUMBER: 37,459
;; REFERENCE/DOCKET NUMBER: DI-1
;; TELECOMMUNICATION INFORMATION:
;; TELEPHONE: 970/493-7272
;; INFORMATION FOR SEQ ID NO: 13:
;; SEQUENCE CHARACTERISTICS:
;; LENGTH: 172 amino acids
;; TYPE: amino acid
;; TOPOLOGY: linear
;; MOLECULE TYPE: protein
;; SEQUENCE DESCRIPTION: SEQ ID NO: 13:
US-09-944-277A-13

Query Match 100.0%; Score 947; DB 4; Length 172;
Best Local Similarity 100.0%; Pred. No. 3e-86; 0; Indels 0; Gaps 0;
Matches 172; Conservative 0; Mismatches 0;

QY 1 VPQPKVSLNPPNRIKGENVLTCTGNNFFVSTKWFHNGSLSEETNSSLNIVNAKF 60
Db 1 VPQPKVSLNPPNRIKGENVLTCTGNNFFVSTKWFHNGSLSEETNSSLNIVNAKF 60

QY 61 EDSEYKCOHQVNESEPVYLEVFSWLLILQASAEVVMGQPLFLRCHGRNWDVYKVIY 120
Db 61 EDSEYKCOHQVNESEPVYLEVFSWLLILQASAEVVMGQPLFLRCHGRNWDVYKVIY 120

QY 121 YKGEALKYWNHNISITNATVEDSGTYCTGKWLQDYSEPLNITVIKA 172
Db 121 YKGEALKYWNHNISITNATVEDSGTYCTGKWLQDYSEPLNITVIKA 172

RESULT 5
US-08-756-387B-11
; Sequence 11, Application US/08756387B
; Patent No. 5945294
; GENERAL INFORMATION:
; APPLICANT: Frank, Glenn R.
; APPLICANT: Porter, James P.
; APPLICANT: Rushlow, Keith E.
; APPLICANT: Wassom, Donald L.
; TITLE OF INVENTION: Method to Detect Ige
; NUMBER OF SEQUENCES: 13
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Carol Talkington Verser, Ph.D.
; STREET: 1825 Sharp Point Drive
; CITY: Fort Collins
; STATE: Colorado
; COUNTRY: USA
; ZIP: 80525
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: Windows 95
; SOFTWARE: Wordperfect for Windows, Version 7.0
; CURRENT APPLICATION DATA:
; FILING DATE: 1999-03-31
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/08/756,387
; FILING DATE: NO. 6309832ember 26, 1996
; ATTORNEY/AGENT INFORMATION:
; NAME: Verser, Carol Talkington
; REGISTRATION NUMBER: 37,459
; REFERENCE/DOCKET NUMBER: DI-1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 970/493-7272
; INFORMATION FOR SEQ ID NO: 11:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 172 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-09-285-873-11

Query Match 100.0%; Score 947; DB 4; Length 197;
Best Local Similarity 100.0%; Pred. No. 3.6e-86;
Matches 172; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

;; LENGTH: 197 amino acids
;; TYPE: amino acid
;; TOPOLOGY: linear
;; MOLECULE TYPE: protein
US-08-756-387B-11

Query Match 100.0%; Score 947; DB 2; Length 197;
Best Local Similarity 100.0%; Pred. No. 3.6e-86;
Matches 172; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 VPQPKVSLNPPNRIKGENVLTCTGNNFFVSTKWFHNGSLSEETNSSLNIVNAKF 60
Db 26 VPQPKVSLNPPNRIKGENVLTCTGNNFFVSTKWFHNGSLSEETNSSLNIVNAKF 85

QY 61 EDSEYKCOHQVNESEPVYLEVFSWLLILQASAEVVMGQPLFLRCHGRNWDVYKVIY 120
Db 86 EDSEYKCOHQVNESEPVYLEVFSWLLILQASAEVVMGQPLFLRCHGRNWDVYKVIY 145

QY 121 YKGEALKYWNHNISITNATVEDSGTYCTGKWLQDYSEPLNITVIKA 172
Db 146 YKGEALKYWNHNISITNATVEDSGTYCTGKWLQDYSEPLNITVIKA 197

RESULT 6
US-09-285-873-11
; Sequence 11, Application US/09285873
; Patent No. 6309832
; GENERAL INFORMATION:
; APPLICANT: Frank, Glenn R.
; APPLICANT: Porter, James P.
; APPLICANT: Rushlow, Keith E.
; APPLICANT: Wassom, Donald L.
; TITLE OF INVENTION: Method to Detect Ige
; NUMBER OF SEQUENCES: 13
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Carol Talkington Verser, Ph.D.
; STREET: 1825 Sharp Point Drive
; CITY: Fort Collins
; STATE: Colorado
; COUNTRY: USA
; ZIP: 80525
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: Windows 95
; SOFTWARE: Wordperfect for Windows, Version 7.0
; CURRENT APPLICATION DATA:
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/08/756,387
; FILING DATE: NO. 6309832ember 26, 1996
; ATTORNEY/AGENT INFORMATION:
; NAME: Verser, Carol Talkington
; REGISTRATION NUMBER: 37,459
; REFERENCE/DOCKET NUMBER: DI-1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 970/493-7272
; INFORMATION FOR SEQ ID NO: 11:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 197 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-09-285-873-11

Query Match 100.0%; Score 947; DB 4; Length 197;
Best Local Similarity 100.0%; Pred. No. 3.6e-86;
Matches 172; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 VPQKPKVSLNPPNRRIFKGENVTLTCNGNPFVSTKWFHNGSLSEETNSLSLNVNAKF 60
Db 26 VPQKPKVSLNPPNRRIFKGENVTLTCNGNPFVSTKWFHNGSLSEETNSLSLNVNAKF 85
QY 61 EDSGEYKCOHQVNESEPVYLEVFSDDLQASAEVVMGQPLFLRCHGWRNWDVYKVIY 120
Db 86 EDSGEYKCOHQVNESEPVYLEVFSDDLQASAEVVMGQPLFLRCHGWRNWDVYKVIY 145
QY 121 YKDGALKWYENHNISITNATVEDSGTYCTGKWQLDYSEPLNITVIKA 172
Db 146 YKDGALKWYENHNISITNATVEDSGTYCTGKWQLDYSEPLNITVIKA 197

RESULT 7

US-09-944-277A-11
; Sequence 11, Application US/09944277A
; Patent No. 6682894

GENERAL INFORMATION:
; APPLICANT: Frank, Glenn R.
; Porter, James P.
; Rushlow, Keith E.
; Wasson, Donald L.

TITLE OF INVENTION: Method to Detect IGE
NUMBER OF SEQUENCES: 13
CORRESPONDENCE ADDRESS:
ADDRESSEE: Carol Talkington Verser, Ph.D.
STREET: 1825 Sharp Point Drive
CITY: Fort Collins
STATE: Colorado
COUNTRY: USA
ZIP: 80525

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: Windows 95
SOFTWARE: WordPerfect for Windows, Version 7.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/944,277A
FILING DATE: 30-Aug-2001
CLASSIFICATION: <unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 09/285,873
FILING DATE: 1999-03-31

ATTORNEY/AGENT INFORMATION:
NAME: Verser, Carol Talkington
REGISTRATION NUMBER: 37,459
REFERENCE/DOCKET NUMBER: DI-1
TELECOMMUNICATION INFORMATION:
TELEPHONE: 970/493-7272
TELEFAX: 970/484-9505

INFORMATION FOR SEQ ID NO: 11:
SEQUENCE CHARACTERISTICS:
LENGTH: 197 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
SEQUENCE DESCRIPTION: SEQ ID NO: 11:
US-09-944-277A-11

Query Match 100.0%; Score 947; DB 4; Length 197;
Best Local Similarity 100.0%; Pred. No. 3.6e-86;
Matches 172; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 VPQKPKVSLNPPNRRIFKGENVTLTCNGNPFVSTKWFHNGSLSEETNSLSLNVNAKF 60
Db 26 VPQKPKVSLNPPNRRIFKGENVTLTCNGNPFVSTKWFHNGSLSEETNSLSLNVNAKF 85
QY 61 EDSGEYKCOHQVNESEPVYLEVFSDDLQASAEVVMGQPLFLRCHGWRNWDVYKVIY 120
Db 86 EDSGEYKCOHQVNESEPVYLEVFSDDLQASAEVVMGQPLFLRCHGWRNWDVYKVIY 145
QY 121 YKDGALKWYENHNISITNATVEDSGTYCTGKWQLDYSEPLNITVIKA 172

Db 146 YKDGALKWYENHNISITNATVEDSGTYCTGKWQLDYSEPLNITVIKA 197

RESULT 8

US-07-869-933-13
; Sequence 13, Application US/07869933
; Patent No. 5770396

GENERAL INFORMATION:
; APPLICANT: KINET, Jean-Pierre

TITLE OF INVENTION: ISOLATION, CHARACTERIZATION, AND USE OF
THE HUMAN B SUBUNIT OF THE HIGH AFFINITY RECEPTOR FOR
IMMUNOGLOBULIN
NUMBER OF SEQUENCES: 34
CORRESPONDENCE ADDRESS:
ADDRESSEE: Foley & Lardner
STREET: 1800 Diagonal Road, Suite 500
CITY: Alexandria
STATE: VA
COUNTRY: USA
ZIP: 22313-0299

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/869,933
FILING DATE: 19920416
CLASSIFICATION: 514

ATTORNEY/AGENT INFORMATION:
NAME: BENT, Stephen A.
REGISTRATION NUMBER: 29,768
REFERENCE/DOCKET NUMBER: 40399/154 NIHD
TELECOMMUNICATION INFORMATION:
TELEPHONE: (703)836-9300
TELEFAX: (703)683-4109
TELEX: 899149

INFORMATION FOR SEQ ID NO: 13:
SEQUENCE CHARACTERISTICS:
LENGTH: 232 amino acids
TYPE: AMINO ACID
TOPOLOGY: linear
MOLECULE TYPE: protein
ORIGINAL SOURCE:
ORGANISM: homo sapien
STRAIN: FcRI alpha subunit
US-07-869-933-13

Query Match 100.0%; Score 947; DB 1; Length 232;
Best Local Similarity 100.0%; Pred. No. 4.4e-86;
Matches 172; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 VPQKPKVSLNPPNRRIFKGENVTLTCNGNPFVSTKWFHNGSLSEETNSLSLNVNAKF 60
Db 1 VPQKPKVSLNPPNRRIFKGENVTLTCNGNPFVSTKWFHNGSLSEETNSLSLNVNAKF 60
QY 61 EDSGEYKCOHQVNESEPVYLEVFSDDLQASAEVVMGQPLFLRCHGWRNWDVYKVIY 120
Db 61 EDSGEYKCOHQVNESEPVYLEVFSDDLQASAEVVMGQPLFLRCHGWRNWDVYKVIY 120
QY 121 YKDGALKWYENHNISITNATVEDSGTYCTGKWQLDYSEPLNITVIKA 172
Db 121 YKDGALKWYENHNISITNATVEDSGTYCTGKWQLDYSEPLNITVIKA 172

RESULT 9

US-08-756-387B-6
; Sequence 6, Application US/08756387B
; Patent No. 5945294

GENERAL INFORMATION:
; APPLICANT: Frank, Glenn R.
; APPLICANT: Porter, James P.


```

; APPLICANT: Rushlow, Keith E.
; APPLICANT: Wassom, Donald L.
; TITLE OF INVENTION: Method to Detect IGE
; NUMBER OF SEQUENCES: 13
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Carol Talkington Verser, Ph.D.
; ADDRESSEE: Heska Corporation
; STREET: 1825 Sharp Point Drive
; CITY: Fort Collins
; STATE: Colorado
; COUNTRY: USA
; ZIP: 80525
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: Windows 95
; SOFTWARE: WordPerfect for Windows, Version 7.0
; CURRENT APPLICATION DATA:
; FILING DATE: US/08/756,387B
; FILING DATE: No. 5945294ember 26, 1996
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Verser, Carol Talkington
; REGISTRATION NUMBER: 37,459
; REFERENCE/DOCKET NUMBER: DI-1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 970/493-7272
; TELEFAX: 970/484-9505
; INFORMATION FOR SEQ ID NO: 6:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 232 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-756-387B-6

Query Match
Best Local Similarity 100.0%; Score 947; DB 2; Length 232;
Matches 172; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 VPQPKVSLNPPWNRIFKGENVLTTCGNNFFVSVSTKWFHNGSLSEETNSSLNIVNAKF 60
DB 1 VPQPKVSLNPPWNRIFKGENVLTTCGNNFFVSVSTKWFHNGSLSEETNSSLNIVNAKF 60
QY 61 EDGGEYKCOHQVNESEPVYLEVFSDWLLQLQASAEVVMGQPLFLRCHGWRNWDVYKVIY 120
DB 61 EDGGEYKCOHQVNESEPVYLEVFSDWLLQLQASAEVVMGQPLFLRCHGWRNWDVYKVIY 120
QY 121 YKDGKALKYWYENHNISITNATVEDSGTYTCTGKWQLDYSEPLNITVIKA 172
DB 121 YKDGKALKYWYENHNISITNATVEDSGTYTCTGKWQLDYSEPLNITVIKA 172

RESULT 11
US-09-285-873-6
; Sequence 6, Application US/09285873
; Patent No. 6309832
; GENERAL INFORMATION:
; APPLICANT: Frank, Glenn R.
; APPLICANT: Porter, James P.
; APPLICANT: Rushlow, Keith E.
; APPLICANT: Wassom, Donald L.
; TITLE OF INVENTION: Method to Detect IGE
; NUMBER OF SEQUENCES: 13
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Carol Talkington Verser, Ph.D.
; ADDRESSEE: Heska Corporation
; STREET: 1825 Sharp Point Drive
; CITY: Fort Collins
; STATE: Colorado
; COUNTRY: USA
; ZIP: 80525
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: Windows 95
; SOFTWARE: WordPerfect for Windows, Version 7.0
; CURRENT APPLICATION DATA:
; FILING DATE: US/09/285,873
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/08/756,387
; FILING DATE: No. 6309832ember 26, 1996
; ATTORNEY/AGENT INFORMATION:
; NAME: Verser, Carol Talkington
; REGISTRATION NUMBER: 37,459
; REFERENCE/DOCKET NUMBER: DI-1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 970/493-7272
; TELEFAX: 970/484-9505
; INFORMATION FOR SEQ ID NO: 6:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 232 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-09-285-873-6

Query Match
Best Local Similarity 100.0%; Score 947; DB 4; Length 232;
Matches 172; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 VPQPKVSLNPPWNRIFKGENVLTTCGNNFFVSVSTKWFHNGSLSEETNSSLNIVNAKF 60
DB 1 VPQPKVSLNPPWNRIFKGENVLTTCGNNFFVSVSTKWFHNGSLSEETNSSLNIVNAKF 60
QY 61 EDGGEYKCOHQVNESEPVYLEVFSDWLLQLQASAEVVMGQPLFLRCHGWRNWDVYKVIY 120
DB 61 EDGGEYKCOHQVNESEPVYLEVFSDWLLQLQASAEVVMGQPLFLRCHGWRNWDVYKVIY 120
QY 121 YKDGKALKYWYENHNISITNATVEDSGTYTCTGKWQLDYSEPLNITVIKA 172
DB 121 YKDGKALKYWYENHNISITNATVEDSGTYTCTGKWQLDYSEPLNITVIKA 172

RESULT 10
US-09-103-663-13
; Sequence 13, Application US/09103663D
; Patent No. 6171803
; GENERAL INFORMATION:
; APPLICANT: Kinet et al.
; TITLE OF INVENTION: Isolation, characterization, and use of the human beta
; TITLE OF INVENTION: subunit of the high affinity receptor for
; TITLE OF INVENTION: immunoglobulin E.
; FILE REFERENCE: 50490
; CURRENT APPLICATION NUMBER: US/09/103,663D
; CURRENT FILING DATE: 1998-06-23
; EARLIER APPLICATION NUMBER: 07/869,933
; EARLIER FILING DATE: 1992-04-16
; NUMBER OF SEQ ID NOS: 35
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 13
; LENGTH: 232
; TYPE: PRT
; ORGANISM: Homo sapiens

```

QY 61 EDSEYKCOHQVNESEPVYLEVFSDDLLOQASAEVVMGQPLFLRCHGRNWDVYKVIY 120
 Db 61 EDSEYKCOHQVNESEPVYLEVFSDDLLOQASAEVVMGQPLFLRCHGRNWDVYKVIY 120
 QY 121 YKDGKALKWYENHNISITNATVEDSGTYCTGKWKQLDYSEPLNITVIKA 172
 Db 121 YKDGKALKWYENHNISITNATVEDSGTYCTGKWKQLDYSEPLNITVIKA 172

RESULT 12

US-09-944-277A-6

; Sequence 6, Application US/09944277A

; Patent No. 6682894

; GENERAL INFORMATION:

; APPLICANT: Frank, Glenn R.

; Porter, James P.

; Wasson, Donald L.

; TITLE OF INVENTION: Method to Detect Ige

; NUMBER OF SEQUENCES: 13

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: Carol Talkington Verser, Ph.D.

; STREET: 1825 Sharp Point Drive

; CITY: Fort Collins

; STATE: Colorado

; COUNTRY: USA

; ZIP: 80525

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy disk

; COMPUTER: IBM PC compatible

; OPERATING SYSTEM: Windows 95

; SOFTWARE: WordPerfect for Windows, Version 7.0

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/09/944,277A

; FILING DATE: 30-Aug-2001

; CLASSIFICATION: <Unknown>

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: 09/285,873

; FILING DATE: 1999-03-31

; ATTORNEY/AGENT INFORMATION:

; NAME: Verser, Carol Talkington

; REGISTRATION NUMBER: 37,459

; REFERENCE/DOCKET NUMBER: DI-1

; TELECOMMUNICATION INFORMATION:

; TELEPHONE: 970/493-7272

; TELEFAX: 970/484-9505

; INFORMATION FOR SEQ ID NO: 6:

; SEQUENCE DESCRIPTION: SEQ ID NO: 6:

US-09-944-277A-6

Query Match

Best Local Similarity 100.0%; Score 947; DB 4; Length 232;

Matches 172; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 VPQKPKVSLNPPNRIKGENVTITCGNNFFVSVSTKWFHNGSLSEETNSLNIYNAKF 60
 Db 1 VPQKPKVSLNPPNRIKGENVTITCGNNFFVSVSTKWFHNGSLSEETNSLNIYNAKF 60
 QY 61 EDSEYKCOHQVNESEPVYLEVFSDDLLOQASAEVVMGQPLFLRCHGRNWDVYKVIY 120
 Db 61 EDSEYKCOHQVNESEPVYLEVFSDDLLOQASAEVVMGQPLFLRCHGRNWDVYKVIY 120
 QY 121 YKDGKALKWYENHNISITNATVEDSGTYCTGKWKQLDYSEPLNITVIKA 172
 Db 121 YKDGKALKWYENHNISITNATVEDSGTYCTGKWKQLDYSEPLNITVIKA 172

RESULT 13

US-07-869-933-11

; Sequence 11, Application US/07869933

; Patent No. 5770396

; GENERAL INFORMATION:

; APPLICANT: KINET, Jean-Pierre

; TITLE OF INVENTION: ISOLATION, CHARACTERIZATION, AND USE OF

; TITLE OF INVENTION: THE HUMAN B SUBUNIT OF THE HIGH AFFINITY RECEPTOR FOR

; NUMBER OF SEQUENCES: 34

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: Foley & Lardner

; STREET: 1800 Diagonal Road, Suite 500

; CITY: Alexandria

; STATE: VA

; COUNTRY: USA

; ZIP: 22313-0299

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy disk

; COMPUTER: IBM PC compatible

; OPERATING SYSTEM: PC-DOS/MS-DOS

; SOFTWARE: Patent In Release #1.0, Version #1.25

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/07/869,933

; FILING DATE: 19920416

; CLASSIFICATION: 514

; ATTORNEY/AGENT INFORMATION:

; NAME: BENT, Stephen A.

; REGISTRATION NUMBER: 29,768

; REFERENCE/DOCKET NUMBER: 40399/154 NIHD

; TELECOMMUNICATION INFORMATION:

; TELEPHONE: (703)836-9300

; TELEFAX: (703)683-4109

; TELEX: 899149

; INFORMATION FOR SEQ ID NO: 11:

; SEQUENCE CHARACTERISTICS:

; LENGTH: 257 amino acids

; TYPE: AMINO ACID

; TOPOLOGY: linear

; MOLECULE TYPE: protein

US-07-869-933-11

Query Match

Best Local Similarity 100.0%; Score 947; DB 1; Length 257;

Matches 172; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 VPQKPKVSLNPPNRIKGENVTITCGNNFFVSVSTKWFHNGSLSEETNSLNIYNAKF 60
 Db 26 VPQKPKVSLNPPNRIKGENVTITCGNNFFVSVSTKWFHNGSLSEETNSLNIYNAKF 85
 QY 61 EDSEYKCOHQVNESEPVYLEVFSDDLLOQASAEVVMGQPLFLRCHGRNWDVYKVIY 120
 Db 86 EDSEYKCOHQVNESEPVYLEVFSDDLLOQASAEVVMGQPLFLRCHGRNWDVYKVIY 145
 QY 121 YKDGKALKWYENHNISITNATVEDSGTYCTGKWKQLDYSEPLNITVIKA 172
 Db 146 YKDGKALKWYENHNISITNATVEDSGTYCTGKWKQLDYSEPLNITVIKA 197

RESULT 14

US-08-756-387B-2

; Sequence 2, Application US/08756387B

; Patent No. 5945294

; GENERAL INFORMATION:

; APPLICANT: Frank, Glenn R.

; APPLICANT: Porter, James P.

; APPLICANT: Rushlow, Keith E.

; APPLICANT: Wasson, Donald L.

; TITLE OF INVENTION: Method to Detect Ige

; NUMBER OF SEQUENCES: 13

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: Carol Talkington Verser, Ph.D.

; ADDRESSEE: Heska Corporation

Db 26 VPQPKVSLNPPWNRIFKGENVTLCNGNNFFVSVSTKWFHNGSLSEETNSSLNIVNAKF 85
Qy 61 EDGSEYKCOHQOVNESEPVILEVPSDWLLILOASAEVVMGQPLFLRCHGWRNWDVYKVIY 120
Db 86 EDGSEYKCOHQOVNESEPVILEVPSDWLLILOASAEVVMGQPLFLRCHGWRNWDVYKVIY 145
Qy 121 YKDGKALKYWEHNHISITNATVEDSGTYCTGKVWQLDYSEPLNITVIKA 172
Db 146 YKDGKALKYWEHNHISITNATVEDSGTYCTGKVWQLDYSEPLNITVIKA 197

Search completed: October 6, 2004, 09:04:38
Job time : 11.2261 secs

STREET: 1825 Sharp Point Drive
CITY: Fort Collins
STATE: Colorado
COUNTRY: USA
ZIP: 80525
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: Windows 95
SOFTWARE: WordPerfect for Windows, Version 7.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/756,387B
FILING DATE: No. 5945294ember 26, 1996
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Verser, Carol Talkington
REGISTRATION NUMBER: 37,459
REFERENCE/DOCKET NUMBER: DI-1
TELECOMMUNICATION INFORMATION:
TELEPHONE: 970/493-7272
TELEFAX: 970/484-9505
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 257 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-756-387B-2

Query Match 100.0%; Score 947; DB 2; Length 257;
Best Local Similarity 100.0%; Pred. No. 5.1e-86;
Matches 172; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 VPQPKVSLNPPWNRIFKGENVTLCNGNNFFVSVSTKWFHNGSLSEETNSSLNIVNAKF 60
Db 26 VPQPKVSLNPPWNRIFKGENVTLCNGNNFFVSVSTKWFHNGSLSEETNSSLNIVNAKF 85
Qy 61 EDGSEYKCOHQOVNESEPVILEVPSDWLLILOASAEVVMGQPLFLRCHGWRNWDVYKVIY 120
Db 86 EDGSEYKCOHQOVNESEPVILEVPSDWLLILOASAEVVMGQPLFLRCHGWRNWDVYKVIY 145
Qy 121 YKDGKALKYWEHNHISITNATVEDSGTYCTGKVWQLDYSEPLNITVIKA 172
Db 146 YKDGKALKYWEHNHISITNATVEDSGTYCTGKVWQLDYSEPLNITVIKA 197

RESULT 15
US-09-103-663-11
; Sequence 11, Application US/09103663D
; Patent No. 6171803
; GENERAL INFORMATION:
; APPLICANT: Kinet et al.
; TITLE OF INVENTION: Isolation, characterization, and use of the human beta
; TITLE OF INVENTION: subunit of the high affinity receptor for
; TITLE OF INVENTION: immunoglobulin E.
; FILE REFERENCE: 50490
; CURRENT APPLICATION NUMBER: US/09/103,663D
; CURRENT FILING DATE: 1998-06-23
; EARLIER APPLICATION NUMBER: 07/869,933
; EARLIER FILING DATE: 1992-04-16
; NUMBER OF SEQ ID NOS: 35
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 11
; LENGTH: 257
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-103-663-11

Query Match 100.0%; Score 947; DB 3; Length 257;
Best Local Similarity 100.0%; Pred. No. 5.1e-86;
Matches 172; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 VPQPKVSLNPPWNRIFKGENVTLCNGNNFFVSVSTKWFHNGSLSEETNSSLNIVNAKF 60

This Page Blank (uspto)

GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.

OM protein - protein search, using sw model

Run on: October 6, 2004, 09:03:44 ; Search time 52.5221 Seconds
(without alignments)
1053.831 Million cell updates/sec

Title: US-10-763-400-13
Perfect score: 947
Sequence: 1 VFQKPKVSLNPWNIFKGE.....GKWLQDYSEPLNITVIKA 172

Scoring table: BLOSUM62
Gapop 10.0 , Capext 0.5

Searched: 1351062 seqs, 321799191 residues

Total number of hits satisfying chosen parameters: 1351062

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Published Applications AA:*
1: /cgn2_6/prodata/2/pubpaa/US07_PUBCOMB.pep.*
2: /cgn2_6/prodata/2/pubpaa/PCT_NEW_PUB.pep.*
3: /cgn2_6/prodata/2/pubpaa/US06_NEW_PUB.pep.*
4: /cgn2_6/prodata/2/pubpaa/US06_PUBCOMB.pep.*
5: /cgn2_6/prodata/2/pubpaa/US07_NEW_PUB.pep.*
6: /cgn2_6/prodata/2/pubpaa/PCTUS_PUBCOMB.pep.*
7: /cgn2_6/prodata/2/pubpaa/US08_NEW_PUB.pep.*
8: /cgn2_6/prodata/2/pubpaa/US08_PUBCOMB.pep.*
9: /cgn2_6/prodata/2/pubpaa/US09A_PUBCOMB.pep.*
10: /cgn2_6/prodata/2/pubpaa/US09B_PUBCOMB.pep.*
11: /cgn2_6/prodata/2/pubpaa/US09C_PUBCOMB.pep.*
12: /cgn2_6/prodata/2/pubpaa/US09_NEW_PUB.pep.*
13: /cgn2_6/prodata/2/pubpaa/US10A_PUBCOMB.pep.*
14: /cgn2_6/prodata/2/pubpaa/US10B_PUBCOMB.pep.*
15: /cgn2_6/prodata/2/pubpaa/US10C_PUBCOMB.pep.*
16: /cgn2_6/prodata/2/pubpaa/US10_NEW_PUB.pep.*
17: /cgn2_6/prodata/2/pubpaa/US10_NEW_PUB.pep.*
18: /cgn2_6/prodata/2/pubpaa/US60_PUBCOMB.pep.*
19: /cgn2_6/prodata/2/pubpaa/US60_PUBCOMB.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	947	100.0	172	9	US-09-944-277A-13
2	947	100.0	172	9	US-09-245-764-9
3	947	100.0	172	12	US-10-293-992-4
4	947	100.0	172	12	US-10-687-109-9
5	947	100.0	176	10	US-09-809-715-2
6	947	100.0	176	12	US-10-293-992-2
7	947	100.0	197	9	US-09-944-277A-11
8	947	100.0	232	9	US-09-944-277A-6
9	947	100.0	257	9	US-09-944-277A-2
10	947	100.0	257	12	US-10-236-392-28
11	947	100.0	257	14	US-10-384-850-45
12	922	97.4	176	10	US-09-809-715-4
13	714.5	75.4	218	12	US-10-236-392-30
14	570	60.2	201	15	US-10-434-817-12
15	570	60.2	236	15	US-10-434-817-7

16	570	60.2	255	15	US-10-434-817-2
17	376.5	39.8	357	14	US-10-027-736A-9
18	374.5	39.5	336	14	US-10-027-736A-65
19	374.5	39.5	374	12	US-09-836-544-23
20	374.5	39.5	374	14	US-10-027-736A-10
21	371.5	39.2	374	14	US-10-308-279-30
22	371.5	39.2	374	14	US-10-384-850-14
23	369	39.0	404	15	US-10-193-377-7
24	367.5	38.8	399	9	US-09-925-301-1128
25	367.5	38.8	399	14	US-10-106-698-5782
26	366	38.6	254	15	US-10-449-566-117
27	362	38.2	233	15	US-10-193-377-6
28	361	38.1	210	15	US-10-449-566-29
29	361	38.1	254	14	US-10-384-850-44
30	361	38.1	254	14	US-10-027-736A-21
31	361	38.1	254	15	US-10-449-566-116
32	360	38.0	234	14	US-10-027-736A-69
33	360	39.0	254	14	US-10-027-736A-20
34	357	37.7	174	9	US-09-245-764-8
35	357	37.7	174	12	US-10-687-109-8
36	357	37.7	261	9	US-09-245-764-7
37	357	37.7	261	12	US-10-687-109-7
38	353	37.3	298	16	US-10-322-696-93
39	348	36.7	252	14	US-10-027-736A-68
40	348	36.7	294	14	US-10-027-736A-18
41	343	36.2	282	14	US-10-027-736A-66
42	343	36.2	310	14	US-10-027-736A-15
43	339	35.8	281	14	US-10-027-736A-67
44	339	35.8	316	14	US-10-027-736A-17
45	335	35.4	170	9	US-09-245-764-6

ALIGNMENTS

RESULT 1
US-09-944-277A-13
; Sequence 13, Application US/09944/277A
; Patent No. US2002034771A1
; GENERAL INFORMATION:
; APPLICANT: Frank, Glenn R.
; Porter, James P.
; Rashlow, Keith E.
; Wassom, Donald L.
; TITLE OF INVENTION: Method to Detect IGE
; NUMBER OF SEQUENCES: 13
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Carol Talkington Verser, Ph.D.
; STREET: 1825 Sharp Point Drive
; City: Fort Collins
; STATE: Colorado
; COUNTRY: USA
; ZIP: 80525
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: Windows 95
; SOFTWARE: WordPerfect for Windows, Version 7.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/944,277A
; FILING DATE: 30-Aug-2001
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 09/285,873
; FILING DATE: 1999-03-31
; ATTORNEY/AGENT INFORMATION:
; NAME: Verser, Carol Talkington
; REGISTRATION NUMBER: 37,459
; REFERENCE/DOCKET NUMBER: DI-1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 970/493-7272
; TELEFAX: 970/484-9505

INFORMATION FOR SEQ ID NO: 13:
SEQUENCE CHARACTERISTICS:
LENGTH: 172 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
SEQUENCE DESCRIPTION: SEQ ID NO: 13:
US-09-944-277A-13

Query Match 100.0%; Score 947; DB 9; Length 172;
Best Local Similarity 100.0%; Pred. No. 4.2e-78;
Matches 172; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 VPQPKVSLNPPNRIFKGNVTLTCGNNTFFVSTKWFHNGSLSEETNSLNIIVNAKF 60
DB 1 VPQPKVSLNPPNRIFKGNVTLTCGNNTFFVSTKWFHNGSLSEETNSLNIIVNAKF 60

QY 61 EDGSEYKCOHQOVNESEPVYLEVFSDDLLOASAEVVMGQPLFLRCHGRNWDVYKVIY 120
DB 61 EDGSEYKCOHQOVNESEPVYLEVFSDDLLOASAEVVMGQPLFLRCHGRNWDVYKVIY 120

QY 121 YKDGALKYWNHNHISITNATVDSGTYYCTGKWQLDYSEPLNITVIKA 172
DB 121 YKDGALKYWNHNHISITNATVDSGTYYCTGKWQLDYSEPLNITVIKA 172

RESULT 2

US-09-245-764-9
Sequence 9, Application US/09245764
Patent No. US20020107359A1

GENERAL INFORMATION:
APPLICANT: Hogarth, P. Mark
APPLICANT: Powell, Maree S.
APPLICANT: McKenzie, Ian F.C.
APPLICANT: Maxwell, Kelly F.
APPLICANT: Garrett, Thomas P.J.
APPLICANT: Epa, Vidana
TITLE OF INVENTION: THREE DIMENSIONAL STRUCTURES AND MODELS OF PC RECEPTORS
TITLE OF INVENTION: AND USES THEREOF
FILE REFERENCE: 4102-4
CURRENT APPLICATION NUMBER: US/09/245,764
CURRENT FILING DATE: 1999-02-05
EARLIER APPLICATION NUMBER: 60/099,994
EARLIER FILING DATE: 1998-09-11
EARLIER APPLICATION NUMBER: 60/073,972
EARLIER FILING DATE: 1998-02-06
NUMBER OF SEQ ID NOS: 15
SOFTWARE: Patent In Ver. 2.0
SEQ ID NO 9
LENGTH: 172
TYPE: PRT
ORGANISM: Homo sapiens
US-09-245-764-9

Query Match 100.0%; Score 947; DB 9; Length 172;
Best Local Similarity 100.0%; Pred. No. 4.2e-78;
Matches 172; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 VPQPKVSLNPPNRIFKGNVTLTCGNNTFFVSTKWFHNGSLSEETNSLNIIVNAKF 60
DB 1 VPQPKVSLNPPNRIFKGNVTLTCGNNTFFVSTKWFHNGSLSEETNSLNIIVNAKF 60

QY 61 EDGSEYKCOHQOVNESEPVYLEVFSDDLLOASAEVVMGQPLFLRCHGRNWDVYKVIY 120
DB 61 EDGSEYKCOHQOVNESEPVYLEVFSDDLLOASAEVVMGQPLFLRCHGRNWDVYKVIY 120

QY 121 YKDGALKYWNHNHISITNATVDSGTYYCTGKWQLDYSEPLNITVIKA 172
DB 121 YKDGALKYWNHNHISITNATVDSGTYYCTGKWQLDYSEPLNITVIKA 172

RESULT 3

US-10-293-992-4

Sequence 4, Application US/10293992
Publication No. US20040033527A1

GENERAL INFORMATION:
APPLICANT: Jaretzky, Theodore S.
APPLICANT: Garman, Scott Clayton
APPLICANT: Kinet, Jean-Pierre
TITLE OF INVENTION: METHODS OF USING A THREE-DIMENSIONAL MODEL OF A PC EPSILON RECEPTOR
TITLE OF INVENTION: CHAIN
FILE REFERENCE: AL-3-CJ-1
CURRENT APPLICATION NUMBER: US/10/293,992
CURRENT FILING DATE: 2002-11-13
PRIOR APPLICATION NUMBER: 09/434,193
PRIOR FILING DATE: 1999-11-04
PRIOR APPLICATION NUMBER: 60/107,219
PRIOR FILING DATE: 1998-11-05
NUMBER OF SEQ ID NOS: 6
SOFTWARE: Patent In version 3.1
SEQ ID NO 4
LENGTH: 172
TYPE: PRT
ORGANISM: Homo sapiens
US-10-293-992-4

Query Match 100.0%; Score 947; DB 12; Length 172;
Best Local Similarity 100.0%; Pred. No. 4.2e-78;
Matches 172; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 VPQPKVSLNPPNRIFKGNVTLTCGNNTFFVSTKWFHNGSLSEETNSLNIIVNAKF 60
DB 1 VPQPKVSLNPPNRIFKGNVTLTCGNNTFFVSTKWFHNGSLSEETNSLNIIVNAKF 60

QY 61 EDGSEYKCOHQOVNESEPVYLEVFSDDLLOASAEVVMGQPLFLRCHGRNWDVYKVIY 120
DB 61 EDGSEYKCOHQOVNESEPVYLEVFSDDLLOASAEVVMGQPLFLRCHGRNWDVYKVIY 120

QY 121 YKDGALKYWNHNHISITNATVDSGTYYCTGKWQLDYSEPLNITVIKA 172
DB 121 YKDGALKYWNHNHISITNATVDSGTYYCTGKWQLDYSEPLNITVIKA 172

RESULT 4

US-10-687-109-9
Sequence 9, Application US/10687109
Publication No. US20040054480A1

GENERAL INFORMATION:
APPLICANT: Hogarth, P. Mark
APPLICANT: Powell, Maree S.
APPLICANT: McKenzie, Ian F.C.
APPLICANT: Maxwell, Kelly F.
APPLICANT: Garrett, Thomas P.J.
APPLICANT: Epa, Vidana
TITLE OF INVENTION: THREE DIMENSIONAL STRUCTURES AND MODELS OF PC RECEPTORS
TITLE OF INVENTION: AND USES THEREOF
FILE REFERENCE: 4102-4
CURRENT APPLICATION NUMBER: US/10/687,109
CURRENT FILING DATE: 2003-10-15
PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: US/09/245,764
PRIOR FILING DATE: EARLIER FILING DATE: 1999-02-05
PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 60/099,994
PRIOR FILING DATE: EARLIER FILING DATE: 1998-09-11
PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 60/073,972
PRIOR FILING DATE: EARLIER FILING DATE: 1998-02-06
NUMBER OF SEQ ID NOS: 15
SOFTWARE: Patent In Ver. 2.0
SEQ ID NO 9
LENGTH: 172
TYPE: PRT
ORGANISM: Homo sapiens
US-10-687-109-9

Query Match 100.0%; Score 947; DB 12; Length 172;
Best Local Similarity 100.0%; Pred. No. 4.2e-78;
Matches 172; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 VPQPKVSLNPPWNRIFKGENVLTTCNGNFFVSSTKWPHNGSLSEETNSSLNINAKF 60
DB 1 VPQPKVSLNPPWNRIFKGENVLTTCNGNFFVSSTKWPHNGSLSEETNSSLNINAKF 60
QY 61 EDSGEYKCHQOVNESEPVYLEVFSDDLQASAEVVMGQPLFLRCHGWRNWDVYKVIY 120
DB 61 EDSGEYKCHQOVNESEPVYLEVFSDDLQASAEVVMGQPLFLRCHGWRNWDVYKVIY 120
QY 121 YKDGALKYWTENHNSITNATVEDSGTYCTGKQWQLDYSEPLNITVIKA 172
DB 121 YKDGALKYWTENHNSITNATVEDSGTYCTGKQWQLDYSEPLNITVIKA 172

RESULT 5

US-09-809-715-2
; Sequence 2, Application US/09809715
; Publication No. US2003003502A1
; GENERAL INFORMATION:
; APPLICANT: Jaretzky, Theodore S.
; APPLICANT: Garman, Scott Clayton
; APPLICANT: Wurzburg, Beth A.
; APPLICANT: Kinet, Jean-Pierre
; TITLE OF INVENTION: THREE-DIMENSIONAL MODEL OF A COMPLEX BETWEEN A FC
; TITLE OF INVENTION: EPSILON RECEPTOR ALPHA CHAIN AND A FC REGION OF AN IGE
; TITLE OF INVENTION: ANTIBODY AND USES THEREOF
; FILE REFERENCE: AL-8
; CURRENT APPLICATION NUMBER: US/09/809,715
; CURRENT FILING DATE: 2001-03-14
; PRIOR APPLICATION NUMBER: 60/189,853
; PRIOR FILING DATE: 2000-03-15
; NUMBER OF SEQ ID NOS: 6
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 2
; LENGTH: 176
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-809-715-2

Query Match 100.0%; Score 947; DB 10; Length 176;
Best Local Similarity 100.0%; Pred. No. 4.3e-78;
Matches 172; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 VPQPKVSLNPPWNRIFKGENVLTTCNGNFFVSSTKWPHNGSLSEETNSSLNINAKF 60
DB 1 VPQPKVSLNPPWNRIFKGENVLTTCNGNFFVSSTKWPHNGSLSEETNSSLNINAKF 60
QY 61 EDSGEYKCHQOVNESEPVYLEVFSDDLQASAEVVMGQPLFLRCHGWRNWDVYKVIY 120
DB 61 EDSGEYKCHQOVNESEPVYLEVFSDDLQASAEVVMGQPLFLRCHGWRNWDVYKVIY 120
QY 121 YKDGALKYWTENHNSITNATVEDSGTYCTGKQWQLDYSEPLNITVIKA 172
DB 121 YKDGALKYWTENHNSITNATVEDSGTYCTGKQWQLDYSEPLNITVIKA 172

RESULT 6

US-10-293-992-2
; Sequence 2, Application US/10293992
; Publication No. US20040033527A1
; GENERAL INFORMATION:
; APPLICANT: Jaretzky, Theodore S.
; APPLICANT: Garman, Scott Clayton
; APPLICANT: Kinet, Jean-Pierre
; TITLE OF INVENTION: METHODS OF USING A THREE-DIMENSIONAL MODEL OF A FC EPSILON RECEPTOR
; TITLE OF INVENTION: CHAIN
; FILE REFERENCE: AL-3-CL-1
; CURRENT APPLICATION NUMBER: US/10/293,992
; CURRENT FILING DATE: 2002-11-13
; PRIOR APPLICATION NUMBER: 09/434,193
; PRIOR FILING DATE: 1999-11-04
; PRIOR APPLICATION NUMBER: 60/107,219
; PRIOR FILING DATE: 1998-11-05

; NUMBER OF SEQ ID NOS: 6
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 2
; LENGTH: 176
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-293-992-2

Query Match 100.0%; Score 947; DB 12; Length 176;
Best Local Similarity 100.0%; Pred. No. 4.3e-78;
Matches 172; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 VPQPKVSLNPPWNRIFKGENVLTTCNGNFFVSSTKWPHNGSLSEETNSSLNINAKF 60
DB 1 VPQPKVSLNPPWNRIFKGENVLTTCNGNFFVSSTKWPHNGSLSEETNSSLNINAKF 60
QY 61 EDSGEYKCHQOVNESEPVYLEVFSDDLQASAEVVMGQPLFLRCHGWRNWDVYKVIY 120
DB 61 EDSGEYKCHQOVNESEPVYLEVFSDDLQASAEVVMGQPLFLRCHGWRNWDVYKVIY 120
QY 121 YKDGALKYWTENHNSITNATVEDSGTYCTGKQWQLDYSEPLNITVIKA 172
DB 121 YKDGALKYWTENHNSITNATVEDSGTYCTGKQWQLDYSEPLNITVIKA 172

RESULT 7

US-09-944-277A-11
; Sequence 11, Application US/09944277A
; Patent No. US20020034771A1
; GENERAL INFORMATION:
; APPLICANT: Frank, Glenn R.
; Porter, James P.
; Rushlow, Keith E.
; Wasson, Donald L.
; TITLE OF INVENTION: Method to Detect Ige
; NUMBER OF SEQUENCES: 13
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Carol Talkington Verser, Ph.D.
; STREET: 1825 Sharp Point Drive
; CITY: Fort Collins
; STATE: Colorado
; COUNTRY: USA
; ZIP: 80525

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: Windows 95
SOFTWARE: WordPerfect for Windows, Version 7.0

CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/944,277A

FILING DATE: 30-Aug-2001

CLASSIFICATION: <Unknown>

PRIOR APPLICATION DATA:
APPLICATION NUMBER: 09/285,873

FILING DATE: 1999-03-31

ATTORNEY/AGENT INFORMATION:
NAME: Verser, Carol Talkington

REGISTRATION NUMBER: 37,459

REFERENCE/DOCKET NUMBER: DI-1

TELECOMMUNICATION INFORMATION:
TELEPHONE: 970/493-7272

TELEFAX: 970/484-9505

INFORMATION FOR SEQ ID NO: 11:
SEQUENCE CHARACTERISTICS:
LENGTH: 197 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
SEQUENCE DESCRIPTION: SEQ ID NO: 11:

US-09-944-277A-11

Query Match 100.0%; Score 947; DB 9; Length 197;

Best Local Similarity 100.0%; Pred. No. 4.9e-78;
Matches 172; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 VPQPKVSLNPPNRIKGENVTLCNGNNFFEVSTKWFHNGSLSEETNSLNIVNAKF 60
Db 26 VPQPKVSLNPPNRIKGENVTLCNGNNFFEVSTKWFHNGSLSEETNSLNIVNAKF 85

QY 61 EDSEYKCOHQVNESEPVYLEVPSDWLLLOASAEVVMGQPLFLRCHGWRNDVYKVIY 120
Db 86 EDSEYKCOHQVNESEPVYLEVPSDWLLLOASAEVVMGQPLFLRCHGWRNDVYKVIY 145

QY 121 YKDGALKWYENHNISITNATVEDSGTYCTGKWQLDYSEPLNITVIKA 172
Db 146 YKDGALKWYENHNISITNATVEDSGTYCTGKWQLDYSEPLNITVIKA 197

RESULT 8
US-09-944-277A-6
; Sequence 6, Application US/09944277A
; Patent No. US20020034771A1
; GENERAL INFORMATION:
; APPLICANT: Frank, Glenn R.
; Porter, James P.
; Rushlow, Keith E.
; Wassom, Donald L.
; TITLE OF INVENTION: Method to Detect Ige
; NUMBER OF SEQUENCES: 13
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Carol Talkington Verser, Ph.D.
; STREET: 1825 Sharp Point Drive
; CITY: Fort Collins
; STATE: Colorado
; COUNTRY: USA
; ZIP: 80525
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: Windows 95
; SOFTWARE: WordPerfect for Windows, Version 7.0
; CURRENT APPLICATION DATA:
; FILING DATE: 30-Aug-2001
; CLASSIFICATION: <unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 09/285,873
; FILING DATE: 1999-03-31
; ATTORNEY/AGENT INFORMATION:
; NAME: Verser, Carol Talkington
; REGISTRATION NUMBER: 37,459
; REFERENCE/DOCKET NUMBER: DI-1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 970/493-7272
; TELEFAX: 970/484-9505
; INFORMATION FOR SEQ ID NO: 6:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 232 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; SEQUENCE DESCRIPTION: SEQ ID NO: 6:
US-09-944-277A-6

Query Match 100.0%; Score 947; DB 9; Length 232;
Best Local Similarity 100.0%; Pred. No. 6e-78;
Matches 172; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 VPQPKVSLNPPNRIKGENVTLCNGNNFFEVSTKWFHNGSLSEETNSLNIVNAKF 60
Db 1 VPQPKVSLNPPNRIKGENVTLCNGNNFFEVSTKWFHNGSLSEETNSLNIVNAKF 60

QY 61 EDSEYKCOHQVNESEPVYLEVPSDWLLLOASAEVVMGQPLFLRCHGWRNDVYKVIY 120

Db 61 EDSEYKCOHQVNESEPVYLEVPSDWLLLOASAEVVMGQPLFLRCHGWRNDVYKVIY 120

QY 121 YKDGALKWYENHNISITNATVEDSGTYCTGKWQLDYSEPLNITVIKA 172
Db 121 YKDGALKWYENHNISITNATVEDSGTYCTGKWQLDYSEPLNITVIKA 172

RESULT 9
US-09-944-277A-2
; Sequence 2, Application US/09944277A
; Patent No. US20020034771A1
; GENERAL INFORMATION:
; APPLICANT: Frank, Glenn R.
; Porter, James P.
; Rushlow, Keith E.
; Wassom, Donald L.
; TITLE OF INVENTION: Method to Detect Ige
; NUMBER OF SEQUENCES: 13
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Carol Talkington Verser, Ph.D.
; STREET: 1825 Sharp Point Drive
; CITY: Fort Collins
; STATE: Colorado
; COUNTRY: USA
; ZIP: 80525
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: Windows 95
; SOFTWARE: WordPerfect for Windows, Version 7.0
; CURRENT APPLICATION DATA:
; FILING DATE: 30-Aug-2001
; CLASSIFICATION: <unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 09/285,873
; FILING DATE: 1999-03-31
; ATTORNEY/AGENT INFORMATION:
; NAME: Verser, Carol Talkington
; REGISTRATION NUMBER: 37,459
; REFERENCE/DOCKET NUMBER: DI-1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 970/493-7272
; TELEFAX: 970/484-9505
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 257 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; SEQUENCE DESCRIPTION: SEQ ID NO: 2:
US-09-944-277A-2

Query Match 100.0%; Score 947; DB 9; Length 257;
Best Local Similarity 100.0%; Pred. No. 6.8e-78;
Matches 172; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 VPQPKVSLNPPNRIKGENVTLCNGNNFFEVSTKWFHNGSLSEETNSLNIVNAKF 60
Db 26 VPQPKVSLNPPNRIKGENVTLCNGNNFFEVSTKWFHNGSLSEETNSLNIVNAKF 85

QY 61 EDSEYKCOHQVNESEPVYLEVPSDWLLLOASAEVVMGQPLFLRCHGWRNDVYKVIY 120
Db 86 EDSEYKCOHQVNESEPVYLEVPSDWLLLOASAEVVMGQPLFLRCHGWRNDVYKVIY 145

QY 121 YKDGALKWYENHNISITNATVEDSGTYCTGKWQLDYSEPLNITVIKA 172
Db 146 YKDGALKWYENHNISITNATVEDSGTYCTGKWQLDYSEPLNITVIKA 197

RESULT 10
US-10-236-392-28

Best Local Similarity 97.7%; Pred. No. 8.1e-76; Matches 168; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 1 VPQKPKVSLNPPNRIKFGENVTLTCGNNFFEVSTKWFHNGSLSEETNSLNIIVNAKF 60
DB 1 VPQKPKVSLNPPNRIKFGENVTLTCGNNFFEVSTKWFHNGSLSEETNSLNIIVNAKF 60

QY 61 EDSGEYKCOHQVNESEPVYLEVFSDDLLOQASAEVVMGQPLFLRCHGWRNWDYKVIY 120
DB 61 EDSGEYKCOHQVNESEPVYLEVFSDDLLOQASAEVVMGQPLFLRCHGWRNWDYKVIY 120

QY 121 YKDGALKYWNHNISITNATVEDSGTYCTGKVMQDLYSEPLNITVIKA 172
DB 121 YKDGALKYWNHNISITNAAEDSGTYCTGKVMQDLYSEPLNITVIKA 172

RESULT 13
US-10-236-392-30
; Sequence 30, Application US/10236392
; Publication No. US20040067490A1
; GENERAL INFORMATION:
; APPLICANT: Anderson, David W
; APPLICANT: Boldog, Ferenc L
; APPLICANT: Burgess, Catherine, E
; APPLICANT: Casman, Stacie J
; APPLICANT: Catterton, Elina
; APPLICANT: Chapoval, Andrei
; APPLICANT: Crabtree, Julie
; APPLICANT: Edinger, Shlomit, R
; APPLICANT: Ellerman, Karen
; APPLICANT: Gorman, Valerie
; APPLICANT: Gorman, Linda
; APPLICANT: Grosse, William M
; APPLICANT: Gusev, Vladimir
; APPLICANT: Kekuda, Ramesh
; APPLICANT: Larochele, William J
; APPLICANT: Li, Li
; APPLICANT: MacDougall, John R
; APPLICANT: Malvankar, Uriel M
; APPLICANT: Miller, Charles E
; APPLICANT: Miller, Isabelle
; APPLICANT: Padigar, Muralidhara
; APPLICANT: Patturajan, Meera
; APPLICANT: Pena, Carol A
; APPLICANT: Peyman, John A
; APPLICANT: Rastelli, Luca
; APPLICANT: Reiger, Daniel K
; APPLICANT: Rothenberg, Mark E
; APPLICANT: Shenoy, Suresh
; APPLICANT: Shimkets, Richard A
; APPLICANT: Smithson, Glennda
; TITLE OF INVENTION: THERAPEUTIC POLYPEPTIDES, NUCLEIC ACIDS ENCODING SAME
; FILE REFERENCE: 21402-442A
; CURRENT APPLICATION NUMBER: US/10/236,392
; CURRENT FILING DATE: 2002-09-06
; PRIOR APPLICATION NUMBER: US09/540,763
; PRIOR FILING DATE: 2000-03-30
; PRIOR APPLICATION NUMBER: US60/390,155
; PRIOR FILING DATE: 2002-06-19
; PRIOR APPLICATION NUMBER: US09/635,949
; PRIOR FILING DATE: 2000-08-10
; PRIOR APPLICATION NUMBER: US60/318,765
; PRIOR FILING DATE: 2001-09-12
; PRIOR APPLICATION NUMBER: US60/357,303
; PRIOR FILING DATE: 2002-02-15
; PRIOR APPLICATION NUMBER: US60/367,753
; PRIOR FILING DATE: 2002-03-25
; PRIOR APPLICATION NUMBER: US60/369,479
; PRIOR FILING DATE: 2002-04-02
; PRIOR APPLICATION NUMBER: US09/659,634
; PRIOR FILING DATE: 2000-09-12
; PRIOR APPLICATION NUMBER: US60/318,120
; PRIOR FILING DATE: 2001-09-07

; PRIOR APPLICATION NUMBER: US60/318,130
; PRIOR FILING DATE: 2001-09-07
; Remaining prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 794
; SOFTWARE: Custom
; SEQ ID NO 30
; LENGTH: 218
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-236-392-30

Query Match 75.4%; Score 714.5; DB 12; Length 218;
Best Local Similarity 77.3%; Pred. No. 7.3e-57;
Matches 133; Conservative 0; Mismatches 0; Indels 39; Gaps 1;

QY 1 VPQKPKVSLNPPNRIKFGENVTLTCGNNFFEVSTKWFHNGSLSEETNSLNIIVNAKF 60
DB 26 VPQKPKVSLNPPNRIKFGENVTLTCGNNFFEVSTKWFHNGSLSEETNSLNIIVNAKF 85

QY 61 EDSGEYKCOHQVNESEPVYLEVFSDDLLOQASAEVVMGQPLFLRCHGWRNWDYKVIY 120
DB 86 EDSGEYK-----CHGWRNWDYKVIY 106

QY 121 YKDGALKYWNHNISITNATVEDSGTYCTGKVMQDLYSEPLNITVIKA 172
DB 107 YKDGALKYWNHNISITNATVEDSGTYCTGKVMQDLYSEPLNITVIKA 158

RESULT 14
US-10-434-817-12
; Sequence 12, Application US/10434817
; Publication No. US20030235579A1
; GENERAL INFORMATION:
; APPLICANT: Weber, Eric R.
; APPLICANT: McCall, Catherine A.
; TITLE OF INVENTION: NOVEL EQUINE FC EPSILON RECEPTOR ALPHA CHAIN NUCLEIC ACID MOLECULES, PROTEINS AND USES THEREOF
; NUMBER OF SEQUENCES: 12
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Heskia Corporation
; STREET: 1825 Sharp Point Drive
; CITY: Fort Collins
; STATE: Colorado
; COUNTRY: USA
; ZIP: 80525
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: WordPerfect for Windows, Version 7.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/10/434,817
; FILING DATE: 08-May-2003
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/09/015,734
; FILING DATE: 29-JAN-1998
; ATTORNEY/AGENT INFORMATION:
; NAME: Verser, Carol Talkington
; REGISTRATION NUMBER: 37,459
; REFERENCE/DOCKET NUMBER: DI-4
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 970/493-7272
; TELEFAX: 970/484-9505
; INFORMATION FOR SEQ ID NO: 12:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 201 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: Protein
; SEQUENCE DESCRIPTION: SEQ ID NO: 12:
US-10-434-817-12

Query Match 60.2%; Score 570; DB 15; Length 201;
Best Local Similarity 62.6%; Pred. No. 8.7e-44;
Matches 109; Conservative 22; Mismatches 39; Indels 4; Gaps 1;

QY 3 QKPKVSLNPPWNRIFKGNVTLTCGNFFVSVSTKWFHNGSLSEETNSLNINAKPED 62
DB 28 RKSTVSLNPPWNRIFKGNVTLTCGNKPLKGNSTWYNTTLEVTSSLNITNASHRS 87

QY 63 SGEYKCOHQVNESEPVYLEVSDWLLQASAEVVMGQPLFRLCHGWRNDVYKVIYK 122
DB 88 SGEYRCRNDLNLSEAVHLEVFSDWLLQASAEVIEGKALVLRGCRGKMDVFKVIYK 147

QY 123 DGEALKYWNHNISITNATVDSGTYYCTG---KVMQLDYESEPLNITVIKA 172
DB 148 DGRPLEYWNKNISIESATTENSGTYCYCEGAFNFKRISERTSDYLNITVKA 201

RESULT 15
US-10-434-817-7
; Sequence 7, Application US/10434817
; Publication No. US20030235579A1
; GENERAL INFORMATION:
; APPLICANT: Weber, Eric R.
; ; McCall, Catherine A.
; TITLE OF INVENTION: NOVEL EQUINE Fc EPSILON RECEPTOR ALPHA
; ; CHAIN NUCLEIC ACID MOLECULES, PROTEINS AND USES THEREOF
; ;
; NUMBER OF SEQUENCES: 12
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Heska Corporation
; STREET: 1825 Sharp Point Drive
; CITY: Fort Collins
; STATE: Colorado
; COUNTRY: USA
; ZIP: 80525
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: WordPerfect for Windows, Version 7.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/10/434,817
; FILING DATE: 08-May-2003
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/09/015,734
; FILING DATE: 29-JAN-1998
; ATTORNEY/AGENT INFORMATION:
; NAME: Verser, Carol Talkington
; REGISTRATION NUMBER: 37,459
; REFERENCE/DOCKET NUMBER: DI-4
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 970/493-7272
; TELEFAX: 970/484-9505
; INFORMATION FOR SEQ ID NO: 7:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 236 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: Protein
; SEQUENCE DESCRIPTION: SEQ ID NO: 7:
US-10-434-817-7

Query Match 60.2%; Score 570; DB 15; Length 236;
Best Local Similarity 62.6%; Pred. No. 1.1e-43;
Matches 109; Conservative 22; Mismatches 39; Indels 4; Gaps 1;

QY 3 QKPKVSLNPPWNRIFKGNVTLTCGNFFVSVSTKWFHNGSLSEETNSLNINAKPED 62
DB 9 RKSTVSLNPPWNRIFKGNVTLTCGNKPLKGNSTWYNTTLEVTSSLNITNASHRS 68

QY 63 SGEYKCOHQVNESEPVYLEVSDWLLQASAEVVMGQPLFRLCHGWRNDVYKVIYK 122
DB 69 SGEYRCRNDLNLSEAVHLEVFSDWLLQASAEVIEGKALVLRGCRGKMDVFKVIYK 128

Qy 123 DGEALKYWNHNISITNATVDSGTYYCTG---KVMQLDYESEPLNITVIKA 172
Db 129 DGRPLEYWNKNISIESATTENSGTYCYCEGAFNFKRISERTSDYLNITVKA 182

Search completed: October 6, 2004, 09:28:11
Job time : 53.5221 secs

This Page Blank (uspro)

GenCore version 5.1.6
Copyright (c) 1993 - 2004 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: October 6, 2004, 09:03:14 : Search time 9.42191 Seconds
(without alignments)
1756.007 Million cell updates/sec

Title: US-10-763-400-13
Perfect score: 947
Sequence: 1 VFQPKVSLNPPNRIKGE.....GKVMQDYSEBPLNITVIKA 172

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283366 seqs, 96191526 residues

Total number of hits satisfying chosen parameters: 283366

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : PIR 78:*

1: pir1:*

2: pir2:*

3: pir3:*

4: pir4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	947	100.0	257	2 S00682	IgE Fc receptor al
2	472	49.8	250	2 A34342	IgE Fc receptor al
3	468	49.4	245	2 A30154	IgE receptor alpha
4	381	40.2	296	2 I46021	Fc-gamma receptor
5	371.5	39.2	344	2 A41357	Fc gamma (15G) rec
6	371.5	39.2	374	1 A39878	Fc gamma (15G) rec
7	371	39.2	280	2 I55577	Fc gamma (15G) rec
8	369	39.0	404	2 A46480	Fc gamma (15G) rec
9	363.5	38.4	336	2 I48471	Fc gamma (15G) rec
10	363	38.3	270	2 A34636	Fc-gamma receptor
11	361	38.1	254	1 J10107	Fc gamma (15G) rec
12	358	37.8	285	2 S36903	Fc gamma (15G) rec
13	357	37.7	233	1 JU0284	Fc gamma (15G) rec
14	354	37.4	283	1 FCMSG1	Fc gamma (15G) rec
15	354	37.4	330	2 A40071	Fc gamma (15G) rec
16	354	37.4	330	2 I49660	Fc-gamma-1/gamma-2
17	353	37.3	267	2 A35902	Fc gamma (15G) rec
18	352	37.2	261	2 S29360	Fc gamma (15G) rec
19	352	37.2	267	2 I56110	Fc-gamma RIIIB-alp
20	338	35.7	160	2 I47163	cytolytic trigger
21	338	35.7	267	2 I72882	Fc gamma receptor
22	335	35.4	323	2 S06946	Fc gamma (15G) rec
23	331	35.0	310	2 J10119	Fc gamma (15G) rec
24	328	34.6	317	2 J10118	Fc gamma (15G) rec
25	327	34.5	157	2 D31327	IgE receptor alpha
26	220	23.2	159	2 I47164	cytolytic trigger
27	161	17.0	1694	2 S50065	sialoadhesin - mou
28	148	15.6	104	2 I47165	cytolytic trigger
29	136.5	14.4	458	1 WMM5K1	biliary glycoprote

30 136.5 14.4 458 2 J15109 biliary glycoprote
31 136.5 14.4 521 2 J15108 biliary glycoprote
32 136.5 14.4 521 2 S34338 biliary glycoprote
33 132 13.9 7962 2 I38346 elastic titin - hu
34 130 13.7 458 2 S23869 cell-adhesion mole
35 130 13.7 458 2 S68177 C-CAM2a protein is
36 130 13.7 519 2 A44783 ecto-ATPase precu
37 129.5 13.7 344 2 A27681 nonspecific cross-
38 126.5 13.4 1239 1 A32579 neuroglian - fruit
39 125 13.2 538 2 J2457 immunoglobulin-lik
40 122 12.9 1327 2 T09402 protein UNC-89 - C
41 120 12.7 6642 2 T29757 cell adhesion prot
42 118 12.5 1033 2 S19247 neural cell adhesi
43 117 12.4 1197 2 T30581 macrophage colony-
44 116.5 12.3 978 2 S16385 heparan sulfate pr
45 116 12.2 3707 2 S18252

ALIGNMENTS

RESULT 1

S00682
IgE Fc receptor alpha chain precursor - human
N:Alternate names: Fc-epsilon receptor
C:Species: Homo sapiens (man)
C:Date: 31-Dec-1988 #sequence_revision 31-Dec-1988 #text_change 23-Jul-1999
C:Accession: S00682; B30154; S42209
R:Kochan, J.; Pettine, L.F.; Hakimi, J.; Kishi, K.; Kinet, J.P.
Nucleic Acids Res. 16, 3584, 1988
A:Title: Isolation of the gene coding for the alpha subunit of the human high affinity I
A:Reference number: S00682; MUID:86233953; PMID:2967464
A:Accession: S00682
A:Molecule type: mRNA
A:Residues: 1-257 <KOC>
A:Cross-references: EMBL:X06948; NID:G31317; PIDN:CAA30025.1; PID:G31318
R:Shimizu, A.; Tepler, I.; Benfey, P.N.; Berenstein, E.H.; Siraganian, R.P.; Leder, P.
Proc. Natl. Acad. Sci. U.S.A. 85, 1907-1911, 1988
A:Title: Human and rat mast cell high-affinity immunoglobulin E receptors: characterizat
A:Reference number: A94191; MUID:88158102; PMID:2964640
A:Accession: B30154
A:Molecule type: mRNA
A:Residues: 1-257 <SHI>
A:Cross-references: GB:J03605; NID:G187449; PIDN:AAA36204.1; PID:G307164
R:Yagi, S.; Yanagida, M.; Tanida, I.; Hasegawa, A.; Okumura, K.; Ra, C.
Eur. J. Biochem. 220, 593-598, 1994
A:Title: High-level expression of the truncated alpha chain of human high-affinity recei
nant product.
A:Reference number: S42209; MUID:94170811; PMID:8125119
A:Accession: S42209
A:Molecule type: protein
A:Residues: 26-197 <YAG>
A:Experimental source: purified recombinant protein
C:Genetics:
A:Gene: GDB:FCER1A
A:Cross-references: GDB:119902; OMIM:147140
A:Map position: 1q23-1q23
C:Superfamily: Fc gamma receptor III; immunoglobulin homology
C:Keywords: immunoglobulin receptor; transmembrane protein
F:1-25/Domain: signal sequence #status predicted <SIG>
F:26-257/Product: IgE Fc receptor alpha chain #status predicted <MAT>
F:44-95/Domain: immunoglobulin homology <IMM1>
F:125-178/Domain: immunoglobulin homology <IMM2>

Query Match 100.0%; Score 947; DB 2; Length 257;

Best Local Similarity 100.0%; Pred. No. 7e-70;

Matches 172; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 VFQPKVSLNPPNRIKGVNLTICNGNFFEVSTKFWFHNGSLSEETNSSLNIVNAKF 60

DB 26 VFQPKVSLNPPNRIKGVNLTICNGNFFEVSTKFWFHNGSLSEETNSSLNIVNAKF 85

QY 61 EDSGEYKCOHQVNESEPVLEVFSDWLLQLQASAEVMEGQPLFLRCHGRWWDVYKVIY 120

```

Db      86 EDGSGYKCHQOVNDESEPVYLEVSDWLLQLQASAEVWVEGQFLRCHGRNWDVYKVIY 145
QY      121 YKDGEALYKYNHNISITNATVDSGYTYCTGKQWQDYSESEPLNITVIKA 172
Db      146 YKDGEALYKYNHNISITNATVDSGYTYCTGKQWQDYSESEPLNITVIKA 197

RESULT 2
A34342
I:GE FC receptor alpha chain precursor - mouse
C:Species: Mus musculus (house mouse)
C>Date: 15-Jun-1990 #sequence_revision 15-Jun-1990 #text_change 23-Jul-1999
C:Accession: A34342; A61238
R:Pa, C.; Jouvin, M.H.E.; Kinet, J.P.
J. Biol. Chem. 264, 15323-15327, 1989
A:Title: Complete structure of the mouse mast cell receptor for IgE (Fc-epsilon-RI) and
A:Reference number: A34342; MUID:89359361; PMID:2527850
A:Accession: A34342
A>Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-250 <RAC>
A:Cross-references: GB:J05018; NID:9193236; PIDN:AAA37600.1; PID:G309224
R:Robertson, M.W.; Mehl, V.S.; Richards, M.L.; Liu, F.T.
Int. Arch. Allergy Appl. Immunol. 96, 289-295, 1991
A:Title: mRNA variants encoding multiple forms of the high-affinity IgE receptor alpha
A:Reference number: A61238; MUID:92234569; PMID:1839735
A:Accession: A61238
A>Status: preliminary
A:Molecule type: DNA
A:Residues: 125-194 <ROB>
C:Superfamily: Fc gamma receptor III; immunoglobulin homology
C:Keywords: alternative splicing; immunoglobulin receptor; transmembrane protein
F:42-94/Domain: immunoglobulin homology <IMM>

Query Match 49.8%; Score 472; DB 2; Length 250;
Best Local Similarity 51.5%; Pred. No. 2.9e-31;
Matches 88; Conservative 35; Mismatches 46; Indels 2; Gaps 2;

QY      3 QKPXVSLNPPNRRIFKGENVTLCNGNFFEV-SSTKWFHNGSLSEETNSLAINVAKPE 61
Db      26 EKSVTLDDPWIRIFTGEKVTLSYGNHLOQMSYTKWINGTVSEVNSHLVIVSATVQ 85

QY      62 DSGYKCHQOVNDESEPVYLEVSDWLLQLQASAEVWVEGQFLRCHGRNWDVYKVIY 121
Db      86 DSGYKICQKGLFKSKPVLNVTQDMLLQTSADMLVHGSFDIRCHGRNWRKVIY 145

QY      122 KDGEALYKYNHNISITNATVDSGYTYCTGKQWQDYSESEPLNITVIKA 172
Db      146 RNDHAFNYSYES-PVSIREATLNDSGTYHCKGYLRQVEYSDKFRIVAVKA 195

RESULT 3
A30154
I:GE receptor alpha chain precursor - rat
K:Alternate names: Fc-epsilon-R alpha chain precursor
C:Species: Rattus norvegicus (Norway rat)
C>Date: 18-Oct-1989 #sequence_revision 18-Oct-1989 #text_change 21-Jan-2000
C:Accession: C31327; A31327; A30154; A27116; I55304
R:Liu, F.T.; Albrandt, K.; Robertson, M.W.
Proc. Natl. Acad. Sci. U.S.A. 85, 5639-5643, 1988
A:Title: cDNA heterogeneity suggests structural variants related to the high-affinity Ig
A:Reference number: A94203; MUID:88289772; PMID:2969594
A:Accession: C31327
A:Molecule type: mRNA
A:Residues: 1-245 <LIU>
A:Cross-references: GB:M21622; GB:J03811
A:Experimental source: basophilic leukemia cell line, clone R3-4
A:Accession: A31327
A:Molecule type: mRNA
A:Residues: 21-245 <LI3>
A:Cross-references: GB:M21622; NID:G204109; PIDN:AAA41146.1; PID:G204110; GB:J03811
A:Experimental source: basophilic leukemia cell line

```

```

R:Shimizu, A.; Tepler, I.; Benfey, P.N.; Berenstein, E.H.; Siraganian, R.P.; Leder, P.
Proc. Natl. Acad. Sci. U.S.A. 85, 1907-1911, 1988
A:Title: Human and rat mast cell high-affinity immunoglobulin E receptors: characterization
A:Reference number: A94191; MUID:88158102; PMID:2964640
A:Accession: A30154
A:Molecule type: mRNA
A:Residues: 1-245 <SHI>
A:Cross-references: GB:J03606; NID:9205331; PIDN:AAA41582.1; PID:G205332
R:Kinet, J.P.; Metzger, H.; Hakimi, J.; Kocan, J.
Biochemistry 26, 4605-4610, 1987
A:Title: A cDNA presumptively coding for the alpha subunit of the receptor with high aff
A:Reference number: A27116; MUID:88024987; PMID:2959318
A:Accession: A27116
A:Molecule type: mRNA
A:Residues: 1-G', 3-236, N', 238-244, 'RLKPNS' <KIN>
R:Tepler, I.; Shimizu, A.; Leder, P.
J. Biol. Chem. 264, 5912-5915, 1989
A:Title: The gene for the rat mast cell high affinity IgE receptor alpha chain. Structur
A:Reference number: I55304; MUID:89174653; PMID:2522441
A:Accession: I55304
A>Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 1-16 <RES>
A:Cross-references: GB:M25334; NID:G341335; PIDN:AAA74562.1; PID:G556391
C:Superfamily: Fc gamma receptor III; immunoglobulin homology
C:Keywords: immunoglobulin receptor; transmembrane protein
F:1-23/Domain: signal sequence #status predicted <SIG>
F:24-245/Product: IgE receptor alpha chain #status predicted <MAT>
F:42-93/Domain: immunoglobulin homology <IMM>

Query Match 49.4%; Score 468; DB 2; Length 245;
Best Local Similarity 50.9%; Pred. No. 6e-31;
Matches 86; Conservative 33; Mismatches 50; Indels 0; Gaps 0;

QY      3 QKPXVSLNPPNRRIFKGENVTLCNGNFFEV-SSTKWFHNGSLSEETNSLAINVAKPE 62
Db      26 QKSVVSLDPPWIRIFTGDKVTLCNGNNSQMNSTKWIHNSISNKSXSHWIVSATIQD 85

QY      63 SGEYKCHQOVNDESEPVYLEVSDWLLQLQASAEVWVEGQFLRCHGRNWDVYKVIY 122
Db      86 SGKYICQKQGYFKSPVLNVTQDMLLQTSADVLDNGSPDIRCSWKWKVHKVIY 145

QY      123 DGEALYKYNHNISITNATVDSGYTYCTGKQWQDYSESEPLNITVIK 171
Db      146 DDIAFKYSYDSNNISIRKATFNDSGYHCTGYLNKVECKSDKFSIAVYK 194

RESULT 4
I46021
Fc-gamma receptor II - bovine
C:Species: Bos primigenius taurus (cattle)
C>Date: 16-Aug-1996 #sequence_revision 16-Aug-1996 #text_change 23-Jul-1999
C:Accession: I46021; S40204
R:Zhang, G.; Young, J.R.; Tregaskes, C.R.; Howard, C.J.
Immunogenetics 39, 423-427, 1994
A:Title: Cattle Fc gamma RI: molecular cloning and ligand specificity.
A:Reference number: I46021; MUID:94245284; PMID:8188320
A:Accession: I46021
A>Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: mRNA
A:Residues: 1-296 <ZHA>
A:Cross-references: EMBL:X75671; NID:9437978; PIDN:CAA53367.1; PID:9437979
C:Superfamily: Fc gamma receptor III; immunoglobulin homology
C:Keywords: immunoglobulin receptor

Query Match 40.2%; Score 381; DB 2; Length 296;
Best Local Similarity 41.2%; Pred. No. 8.8e-24;
Matches 70; Conservative 33; Mismatches 65; Indels 2; Gaps 1;

QY      2 PQPKK--VSLNPPNRRIFKGENVTLCNGNFFEV-SSTKWFHNGSLSEETNSLAINVAK 59
Db      44 PDLKAVVTQAPINVLREDVLTTCQGTSGFAGNLTTFHNGSSHTQKQPSYFRAG 103

```

A;Accession: I70304
A;Status: translated from GB/EMBL/DBJ
A;Molecule type: mRNA
A;Residues: 1-374 <RES>
A;Cross-references: GB:U103418; NID:gl84840; PIDN:AAA36049.1; PID:G292169
R;Allen, J.M.; Seed, B.
Science 243, 378-381, 1989
A;Title: Isolation and expression of functional high-affinity Fc receptor complementary
A;Reference number: A41357; MUID:89100284; PMID:2911749
A;Accession: B41357
A;Molecule type: mRNA
A;Residues: 1-24, 'S', 26-337, 'T', 339-374 <A1>
A;Cross-references: GB:X14356; GB:M21091; NID:g31331; PIDN:CAA32537.1; PID:g31332
R;Allen, J.M.; Seed, B.
Nucleic Acids Res. 16, 11824, 1988
A;Title: Nucleotide sequence of three cDNAs for the human high affinity Fc receptor (FCR)
A;Reference number: S03018; MUID:89098339; PMID:2974947
A;Accession: S03018
A;Molecule type: mRNA
A;Residues: 1-24, 'S', 26-337, 'T', 339-374 <A12>
A;Cross-references: EMBL:X14356; NID:g31331; PIDN:CAA32537.1; PID:g31332
R;Perez, C.; Wietzerbin, J.; Benech, P.D.
Mol. Cell. Biol. 13, 2182-2192, 1993
A;Title: Two cis-DNA elements involved in myeloid-cell-specific expression and gamma in-
ism.
A;Reference number: I57525; MUID:93204964; PMID:8455606
A;Accession: I57525
A;Status: translated from GB/EMBL/DBJ
A;Molecule type: DNA
A;Residues: 1-8 <RES2>
A;Cross-references: GB:S57204; NID:g298692; PIDN:AAD13887.1; PID:g4261587
C;Genetics:
A;Gene: GDB:FCGR1A; CD64
A;Cross-references: GDB:135911; OMIM:146760
A;Map position: 1q21-1q21
A;Superfamily: Fc gamma receptor 1; immunoglobulin homology
C;Keywords: alternative splicing; glycoprotein; immunoglobulin receptor; transmembrane
F;1-15/Domain: signal sequence #status predicted <SIG>
F;16-292/Domain: extracellular #status predicted <EXT>
F;117-170/Domain: immunoglobulin homology <IMM2>
F;293-313/Domain: transmembrane #status predicted <TM>
F;59,78,152,159,163,195,240/Binding site: carbohydrate (Asn) (covalent) #status predicted
Query Match 39,28; Score 371.5; DB 1; Length 374;
Best Local Similarity 41.08; Pred. No. 6.9e-23;
Matches 68; Conservative 3; Mismatches 60; Indels 1; Gaps 1;
Qy 4 KPQVSLPMPNRIKPGENVLTICGNNGNFFEVSSYTKWFHNGSLSEETSSNINVNKPEDS 63
Db 21 KAVITLQPPMVSVFQEEVTTLHCEVLHLPVGSSSTQWFLNGTATQTSTPSRITSASVND 80
Qy 64 GEYKQCHQVNESPVLEVFSFDLLQASAEVMEGQPLFLRCHGWRNWDVYKVIYKD 123
Db 81 GEYRCQGLSGRSPIQLETHRGVLLQVSRVTEGEPLALRCHANKDKLVNVLVYRN 140
Qy 124 GEALKYVENHNISITNATVDSGTYYCTYTKGVQWLDYSEPLNITY 169
Db 141 GKAFKFFHNSNLIILKTNISHNGTYHCSG-MGKHRYTSAGISVTV 185
RESULT 7
I55577
Fc gamma (IgG) receptor I-B splice form 1.precursor - human
N;Alternate names: Cd64
N;Contains: Fc-gamma (IgG) receptor I-B splice form 2
C;Species: Homo sapiens (man)
C;Date: 02-Jul-1996 #sequence_revision 02-Jul-1996 #text_change 21-Jan-2000
C;Accession: I55577; I70303
R;Porces, A.J.; Redecha, P.B.; Doebele, R.; Pan, L.C.; Salmon, J.E.; Kimberly, R.P.
J. Clin. Invest. 90, 2102-2109, 1992
A;Title: Novel Fc gamma receptor I family gene products in human mononuclear cells.
A;Reference number: I55577; MUID:93055454; PMID:1430234
A;Accession: I55577

A>Status: preliminary; translated from GB/EMBL/DBJ
 A:Molecule type: mRNA
 A:Residues: 1-260 <RES>
 A:Cross-references: GB:L03419; NID:G182460; PIDN:AAA35825.1; PID:G292023
 A>Note: splice form B1
 A:Accession: I70303
 A>Status: preliminary; translated from GB/EMBL/DBJ
 A:Molecule type: mRNA
 A:Residues: 1-10, 103-153 'A', 155-280 <RE2>
 A:Cross-references: GB:L03420; NID:G182461; PIDN:AAA35826.1; PID:G292024
 A:Experimental source: mononuclear cells
 A>Note: splice form B2
 A:Comment: This receptor does not bind monomeric IgG with high affinity.
 C:Genetics:
 A:Gene: GDB:FCGR1B; CD64
 A:Cross-references: GDB:135923; OMIM:601502
 A:Map position: lp12-lp12
 C:Superfamily: Fc gamma receptor I; immunoglobulin homology
 C:Keywords: alternative splicing; glycoprotein; immunoglobulin receptor; transmembrane protein
 F:117-170/Domain: immunoglobulin homology <IMM>

Query Match 39.2%; Score 371; DB 2; Length 280;
 Best Local Similarity 43.3%; Pred. No. 5.4e-23; Indels 0; Gaps 0;
 Matches 65; Conservative 32; Mismatches 53

QY 4 KPVSLNPPWNRIPKGENVTITCNNGNFFVSVSTKWFHNGSLSEETNSLNINVAKPEDS 63
 DB 21 KAVITLQPPWVSFQETVTLHCEVLHPGSSSTQWFLNGTATQTSTPSYRITSASVND 80
 QY 64 GEYKCOHQVNESEPVYLEVFSDWLLQASAEVVMGQPLFLRCHGWRNDVYKVIYKD 123
 DB 81 GEYKQRCGLSRSDPQIEIHRGWLQLQVSSRVEGEPLALRCHAWKDLVNVLYRN 140
 QY 124 GEALKYWNHNISITNATVEDSGTYCTGKWKQWLDYSEPLNITV 153
 DB 141 GKAFKFFHNSNLITKLNISHNGTYHCSG 170

RESULT 8
 A46480
 Fc gamma (IgG) receptor high affinity - mouse
 N:Alternative names: high affinity IgG receptor
 C:Species: Mus musculus (house mouse)
 C:Date: 18-Jun-1993 #sequence_revision 18-Nov-1994 #text_change 21-Jan-2000
 C:Accession: A46480; A43511
 R:Osman, N.; Kozak, C.A.; McKenzie, I.F.; Hogarth, P.M.
 J. Immunol. 148, 1570-1575, 1992
 A:Title: Structure and mapping of the gene encoding mouse high affinity Fc gamma RI and J. Immunol. 148, 1570-1575, 1992
 A:Reference number: A46480; MUID:92166399; PMID:1531670
 A:Accession: A46480
 A>Status: preliminary
 A:Molecule type: DNA
 A:Residues: 1-404 <OSM>
 A>Note: sequence extracted from NCBI backbone (NCBIN:85205, NCBIN:85208, NCBIN:85212, NCBI:85215, NCBIN:85216, NCBIN:85217, NCBIN:85218, NCBIN:85219, NCBIN:85220, NCBIN:85221, NCBIN:85222, NCBIN:85223, NCBIN:85224, NCBIN:85225, NCBIN:85226, NCBIN:85227, NCBIN:85228, NCBIN:85229, NCBIN:85230, NCBIN:85231, NCBIN:85232, NCBIN:85233, NCBIN:85234, NCBIN:85235, NCBIN:85236, NCBIN:85237, NCBIN:85238, NCBIN:85239, NCBIN:85240, NCBIN:85241, NCBIN:85242, NCBIN:85243, NCBIN:85244, NCBIN:85245, NCBIN:85246, NCBIN:85247, NCBIN:85248, NCBIN:85249, NCBIN:85250, NCBIN:85251, NCBIN:85252, NCBIN:85253, NCBIN:85254, NCBIN:85255, NCBIN:85256, NCBIN:85257, NCBIN:85258, NCBIN:85259, NCBIN:85260, NCBIN:85261, NCBIN:85262, NCBIN:85263, NCBIN:85264, NCBIN:85265, NCBIN:85266, NCBIN:85267, NCBIN:85268, NCBIN:85269, NCBIN:85270, NCBIN:85271, NCBIN:85272, NCBIN:85273, NCBIN:85274, NCBIN:85275, NCBIN:85276, NCBIN:85277, NCBIN:85278, NCBIN:85279, NCBIN:85280, NCBIN:85281, NCBIN:85282, NCBIN:85283, NCBIN:85284, NCBIN:85285, NCBIN:85286, NCBIN:85287, NCBIN:85288, NCBIN:85289, NCBIN:85290, NCBIN:85291, NCBIN:85292, NCBIN:85293, NCBIN:85294, NCBIN:85295, NCBIN:85296, NCBIN:85297, NCBIN:85298, NCBIN:85299, NCBIN:85300, NCBIN:85301, NCBIN:85302, NCBIN:85303, NCBIN:85304, NCBIN:85305, NCBIN:85306, NCBIN:85307, NCBIN:85308, NCBIN:85309, NCBIN:85310, NCBIN:85311, NCBIN:85312, NCBIN:85313, NCBIN:85314, NCBIN:85315, NCBIN:85316, NCBIN:85317, NCBIN:85318, NCBIN:85319, NCBIN:85320, NCBIN:85321, NCBIN:85322, NCBIN:85323, NCBIN:85324, NCBIN:85325, NCBIN:85326, NCBIN:85327, NCBIN:85328, NCBIN:85329, NCBIN:85330, NCBIN:85331, NCBIN:85332, NCBIN:85333, NCBIN:85334, NCBIN:85335, NCBIN:85336, NCBIN:85337, NCBIN:85338, NCBIN:85339, NCBIN:85340, NCBIN:85341, NCBIN:85342, NCBIN:85343, NCBIN:85344, NCBIN:85345, NCBIN:85346, NCBIN:85347, NCBIN:85348, NCBIN:85349, NCBIN:85350, NCBIN:85351, NCBIN:85352, NCBIN:85353, NCBIN:85354, NCBIN:85355, NCBIN:85356, NCBIN:85357, NCBIN:85358, NCBIN:85359, NCBIN:85360, NCBIN:85361, NCBIN:85362, NCBIN:85363, NCBIN:85364, NCBIN:85365, NCBIN:85366, NCBIN:85367, NCBIN:85368, NCBIN:85369, NCBIN:85370, NCBIN:85371, NCBIN:85372, NCBIN:85373, NCBIN:85374, NCBIN:85375, NCBIN:85376, NCBIN:85377, NCBIN:85378, NCBIN:85379, NCBIN:85380, NCBIN:85381, NCBIN:85382, NCBIN:85383, NCBIN:85384, NCBIN:85385, NCBIN:85386, NCBIN:85387, NCBIN:85388, NCBIN:85389, NCBIN:85390, NCBIN:85391, NCBIN:85392, NCBIN:85393, NCBIN:85394, NCBIN:85395, NCBIN:85396, NCBIN:85397, NCBIN:85398, NCBIN:85399, NCBIN:85400, NCBIN:85401, NCBIN:85402, NCBIN:85403, NCBIN:85404, NCBIN:85405, NCBIN:85406, NCBIN:85407, NCBIN:85408, NCBIN:85409, NCBIN:85410, NCBIN:85411, NCBIN:85412, NCBIN:85413, NCBIN:85414, NCBIN:85415, NCBIN:85416, NCBIN:85417, NCBIN:85418, NCBIN:85419, NCBIN:85420, NCBIN:85421, NCBIN:85422, NCBIN:85423, NCBIN:85424, NCBIN:85425, NCBIN:85426, NCBIN:85427, NCBIN:85428, NCBIN:85429, NCBIN:85430, NCBIN:85431, NCBIN:85432, NCBIN:85433, NCBIN:85434, NCBIN:85435, NCBIN:85436, NCBIN:85437, NCBIN:85438, NCBIN:85439, NCBIN:85440, NCBIN:85441, NCBIN:85442, NCBIN:85443, NCBIN:85444, NCBIN:85445, NCBIN:85446, NCBIN:85447, NCBIN:85448, NCBIN:85449, NCBIN:85450, NCBIN:85451, NCBIN:85452, NCBIN:85453, NCBIN:85454, NCBIN:85455, NCBIN:85456, NCBIN:85457, NCBIN:85458, NCBIN:85459, NCBIN:85460, NCBIN:85461, NCBIN:85462, NCBIN:85463, NCBIN:85464, NCBIN:85465, NCBIN:85466, NCBIN:85467, NCBIN:85468, NCBIN:85469, NCBIN:85470, NCBIN:85471, NCBIN:85472, NCBIN:85473, NCBIN:85474, NCBIN:85475, NCBIN:85476, NCBIN:85477, NCBIN:85478, NCBIN:85479, NCBIN:85480, NCBIN:85481, NCBIN:85482, NCBIN:85483, NCBIN:85484, NCBIN:85485, NCBIN:85486, NCBIN:85487, NCBIN:85488, NCBIN:85489, NCBIN:85490, NCBIN:85491, NCBIN:85492, NCBIN:85493, NCBIN:85494, NCBIN:85495, NCBIN:85496, NCBIN:85497, NCBIN:85498, NCBIN:85499, NCBIN:85500, NCBIN:85501, NCBIN:85502, NCBIN:85503, NCBIN:85504, NCBIN:85505, NCBIN:85506, NCBIN:85507, NCBIN:85508, NCBIN:85509, NCBIN:85510, NCBIN:85511, NCBIN:85512, NCBIN:85513, NCBIN:85514, NCBIN:85515, NCBIN:85516, NCBIN:85517, NCBIN:85518, NCBIN:85519, NCBIN:85520, NCBIN:85521, NCBIN:85522, NCBIN:85523, NCBIN:85524, NCBIN:85525, NCBIN:85526, NCBIN:85527, NCBIN:85528, NCBIN:85529, NCBIN:85530, NCBIN:85531, NCBIN:85532, NCBIN:85533, NCBIN:85534, NCBIN:85535, NCBIN:85536, NCBIN:85537, NCBIN:85538, NCBIN:85539, NCBIN:85540, NCBIN:85541, NCBIN:85542, NCBIN:85543, NCBIN:85544, NCBIN:85545, NCBIN:85546, NCBIN:85547, NCBIN:85548, NCBIN:85549, NCBIN:85550, NCBIN:85551, NCBIN:85552, NCBIN:85553, NCBIN:85554, NCBIN:85555, NCBIN:85556, NCBIN:85557, NCBIN:85558, NCBIN:85559, NCBIN:85560, NCBIN:85561, NCBIN:85562, NCBIN:85563, NCBIN:85564, NCBIN:85565, NCBIN:85566, NCBIN:85567, NCBIN:85568, NCBIN:85569, NCBIN:85570, NCBIN:85571, NCBIN:85572, NCBIN:85573, NCBIN:85574, NCBIN:85575, NCBIN:85576, NCBIN:85577, NCBIN:85578, NCBIN:85579, NCBIN:85580, NCBIN:85581, NCBIN:85582, NCBIN:85583, NCBIN:85584, NCBIN:85585, NCBIN:85586, NCBIN:85587, NCBIN:85588, NCBIN:85589, NCBIN:85590, NCBIN:85591, NCBIN:85592, NCBIN:85593, NCBIN:85594, NCBIN:85595, NCBIN:85596, NCBIN:85597, NCBIN:85598, NCBIN:85599, NCBIN:85600, NCBIN:85601, NCBIN:85602, NCBIN:85603, NCBIN:85604, NCBIN:85605, NCBIN:85606, NCBIN:85607, NCBIN:85608, NCBIN:85609, NCBIN:85610, NCBIN:85611, NCBIN:85612, NCBIN:85613, NCBIN:85614, NCBIN:85615, NCBIN:85616, NCBIN:85617, NCBIN:85618, NCBIN:85619, NCBIN:85620, NCBIN:85621, NCBIN:85622, NCBIN:85623, NCBIN:85624, NCBIN:85625, NCBIN:85626, NCBIN:85627, NCBIN:85628, NCBIN:85629, NCBIN:85630, NCBIN:85631, NCBIN:85632, NCBIN:85633, NCBIN:85634, NCBIN:85635, NCBIN:85636, NCBIN:85637, NCBIN:85638, NCBIN:85639, NCBIN:85640, NCBIN:85641, NCBIN:85642, NCBIN:85643, NCBIN:85644, NCBIN:85645, NCBIN:85646, NCBIN:85647, NCBIN:85648, NCBIN:85649, NCBIN:85650, NCBIN:85651, NCBIN:85652, NCBIN:85653, NCBIN:85654, NCBIN:85655, NCBIN:85656, NCBIN:85657, NCBIN:85658, NCBIN:85659, NCBIN:85660, NCBIN:85661, NCBIN:85662, NCBIN:85663, NCBIN:85664, NCBIN:85665, NCBIN:85666, NCBIN:85667, NCBIN:85668, NCBIN:85669, NCBIN:85670, NCBIN:85671, NCBIN:85672, NCBIN:85673, NCBIN:85674, NCBIN:85675, NCBIN:85676, NCBIN:85677, NCBIN:85678, NCBIN:85679, NCBIN:85680, NCBIN:85681, NCBIN:85682, NCBIN:85683, NCBIN:85684, NCBIN:85685, NCBIN:85686, NCBIN:85687, NCBIN:85688, NCBIN:85689, NCBIN:85690, NCBIN:85691, NCBIN:85692, NCBIN:85693, NCBIN:85694, NCBIN:85695, NCBIN:85696, NCBIN:85697, NCBIN:85698, NCBIN:85699, NCBIN:85700, NCBIN:85701, NCBIN:85702, NCBIN:85703, NCBIN:85704, NCBIN:85705, NCBIN:85706, NCBIN:85707, NCBIN:85708, NCBIN:85709, NCBIN:85710, NCBIN:85711, NCBIN:85712, NCBIN:85713, NCBIN:85714, NCBIN:85715, NCBIN:85716, NCBIN:85717, NCBIN:85718, NCBIN:85719, NCBIN:85720, NCBIN:85721, NCBIN:85722, NCBIN:85723, NCBIN:85724, NCBIN:85725, NCBIN:85726, NCBIN:85727, NCBIN:85728, NCBIN:85729, NCBIN:85730, NCBIN:85731, NCBIN:85732, NCBIN:85733, NCBIN:85734, NCBIN:85735, NCBIN:85736, NCBIN:85737, NCBIN:85738, NCBIN:85739, NCBIN:85740, NCBIN:85741, NCBIN:85742, NCBIN:85743, NCBIN:85744, NCBIN:85745, NCBIN:85746, NCBIN:85747, NCBIN:85748, NCBIN:85749, NCBIN:85750, NCBIN:85751, NCBIN:85752, NCBIN:85753, NCBIN:85754, NCBIN:85755, NCBIN:85756, NCBIN:85757, NCBIN:85758, NCBIN:85759, NCBIN:85760, NCBIN:85761, NCBIN:85762, NCBIN:85763, NCBIN:85764, NCBIN:85765, NCBIN:85766, NCBIN:85767, NCBIN:85768, NCBIN:85769, NCBIN:85770, NCBIN:85771, NCBIN:85772, NCBIN:85773, NCBIN:85774, NCBIN:85775, NCBIN:85776, NCBIN:85777, NCBIN:85778, NCBIN:85779, NCBIN:85780, NCBIN:85781, NCBIN:85782, NCBIN:85783, NCBIN:85784, NCBIN:85785, NCBIN:85786, NCBIN:85787, NCBIN:85788, NCBIN:85789, NCBIN:85790, NCBIN:85791, NCBIN:85792, NCBIN:85793, NCBIN:85794, NCBIN:85795, NCBIN:85796, NCBIN:85797, NCBIN:85798, NCBIN:85799, NCBIN:85800, NCBIN:85801, NCBIN:85802, NCBIN:85803, NCBIN:85804, NCBIN:85805, NCBIN:85806, NCBIN:85807, NCBIN:85808, NCBIN:85809, NCBIN:85810, NCBIN:85811, NCBIN:85812, NCBIN:85813, NCBIN:85814, NCBIN:85815, NCBIN:85816, NCBIN:85817, NCBIN:85818, NCBIN:85819, NCBIN:85820, NCBIN:85821, NCBIN:85822, NCBIN:85823, NCBIN:85824, NCBIN:85825, NCBIN:85826, NCBIN:85827, NCBIN:85828, NCBIN:85829, NCBIN:85830, NCBIN:85831, NCBIN:85832, NCBIN:85833, NCBIN:85834, NCBIN:85835, NCBIN:85836, NCBIN:85837, NCBIN:85838, NCBIN:85839, NCBIN:85840, NCBIN:85841, NCBIN:85842, NCBIN:85843, NCBIN:85844, NCBIN:85845, NCBIN:85846, NCBIN:85847, NCBIN:85848, NCBIN:85849, NCBIN:85850, NCBIN:85851, NCBIN:85852, NCBIN:85853, NCBIN:85854, NCBIN:85855, NCBIN:85856, NCBIN:85857, NCBIN:85858, NCBIN:85859, NCBIN:85860, NCBIN:85861, NCBIN:85862, NCBIN:85863, NCBIN:85864, NCBIN:85865, NCBIN:85866, NCBIN:85867, NCBIN:85868, NCBIN:85869, NCBIN:85870, NCBIN:85871, NCBIN:85872, NCBIN:85873, NCBIN:85874, NCBIN:85875, NCBIN:85876, NCBIN:85877, NCBIN:85878, NCBIN:85879, NCBIN:85880, NCBIN:85881, NCBIN:85882, NCBIN:85883, NCBIN:85884, NCBIN:85885, NCBIN:85886, NCBIN:85887, NCBIN:85888, NCBIN:85889, NCBIN:85890, NCBIN:85891, NCBIN:85892, NCBIN:85893, NCBIN:85894, NCBIN:85895, NCBIN:85896, NCBIN:85897, NCBIN:85898, NCBIN:85899, NCBIN:85900, NCBIN:85901, NCBIN:85902, NCBIN:85903, NCBIN:85904, NCBIN:85905, NCBIN:85906, NCBIN:85907, NCBIN:85908, NCBIN:85909, NCBIN:85910, NCBIN:85911, NCBIN:85912, NCBIN:85913, NCBIN:85914, NCBIN:85915, NCBIN:85916, NCBIN:85917, NCBIN:85918, NCBIN:85919, NCBIN:85920, NCBIN:85921, NCBIN:85922, NCBIN:85923, NCBIN:85924, NCBIN:85925, NCBIN:85926, NCBIN:85927, NCBIN:85928, NCBIN:85929, NCBIN:85930, NCBIN:85931, NCBIN:85932, NCBIN:85933, NCBIN:85934, NCBIN:85935, NCBIN:85936, NCBIN:85937, NCBIN:85938, NCBIN:85939, NCBIN:85940, NCBIN:85941, NCBIN:85942, NCBIN:85943, NCBIN:85944, NCBIN:85945, NCBIN:85946, NCBIN:85947, NCBIN:85948, NCBIN:85949, NCBIN:85950, NCBIN:85951, NCBIN:85952, NCBIN:85953, NCBIN:85954, NCBIN:85955, NCBIN:85956, NCBIN:85957, NCBIN:85958, NCBIN:85959, NCBIN:85960, NCBIN:85961, NCBIN:85962, NCBIN:85963, NCBIN:85964, NCBIN:85965, NCBIN:85966, NCBIN:85967, NCBIN:85968, NCBIN:85969, NCBIN:85970, NCBIN:85971, NCBIN:85972, NCBIN:85973, NCBIN:85974, NCBIN:85975, NCBIN:85976, NCBIN:85977, NCBIN:85978, NCBIN:85979, NCBIN:85980, NCBIN:85981, NCBIN:85982, NCBIN:85983, NCBIN:85984, NCBIN:85985, NCBIN:85986, NCBIN:85987, NCBIN:85988, NCBIN:85989, NCBIN:85990, NCBIN:85991, NCBIN:85992, NCBIN:85993, NCBIN:85994, NCBIN:85995, NCBIN:85996, NCBIN:85997, NCBIN:85998, NCBIN:85999, NCBIN:86000, NCBIN:86001, NCBIN:86002, NCBIN:86003, NCBIN:86004, NCBIN:86005, NCBIN:86006, NCBIN:86007, NCBIN:86008, NCBIN:86009, NCBIN:86010, NCBIN:86011, NCBIN:86012, NCBIN:86013, NCBIN:86014, NCBIN:86015, NCBIN:86016, NCBIN:86017, NCBIN:86018, NCBIN:86019, NCBIN:86020, NCBIN:86021, NCBIN:86022, NCBIN:86023, NCBIN:86024, NCBIN:86025, NCBIN:86026, NCBIN:86027, NCBIN:86028, NCBIN:86029, NCBIN:86030, NCBIN:86031, NCBIN:86032, NCBIN:86033, NCBIN:86034, NCBIN:86035, NCBIN:86036, NCBIN:86037, NCBIN:86038, NCBIN:86039, NCBIN:86040, NCBIN:86041, NCBIN:86042, NCBIN:86043, NCBIN:86044, NCBIN:86045, NCBIN:86046, NCBIN:86047, NCBIN:86048, NCBIN:86049, NCBIN:86050, NCBIN:86051, NCBIN:86052, NCBIN:86053, NCBIN:86054, NCBIN:86055, NCBIN:86056, NCBIN:86057, NCBIN:86058, NCBIN:86059, NCBIN:86060, NCBIN:86061, NCBIN:86062, NCBIN:86063, NCBIN:86064, NCBIN:86065, NCBIN:86066, NCBIN:86067, NCBIN:86068, NCBIN:86069, NCBIN:86070, NCBIN:86071, NCBIN:86072, NCBIN:86073, NCBIN:86074, NCBIN:86075, NCBIN:86076, NCBIN:86077, NCBIN:86078, NCBIN:86079, NCBIN:86080, NCBIN:86081, NCBIN:86082, NCBIN:86083, NCBIN:86084, NCBIN:86085, NCBIN:86086, NCBIN:86087, NCBIN:86088, NCBIN:86089, NCBIN:86090, NCBIN:86091, NCBIN:86092, NCBIN:86093, NCBIN:86094, NCBIN:86095, NCBIN:86096, NCBIN:86097, NCBIN:86098, NCBIN:86099, NCBIN:86100, NCBIN:86101, NCBIN:86102, NCBIN:86103, NCBIN:86104, NCBIN:86105, NCBIN:86106, NCBIN:86107, NCBIN:86108, NCBIN:86109, NCBIN:86110, NCBIN:86111, NCBIN:86112, NCBIN:86113, NCBIN:86114, NCBIN:86115, NCBIN:86116, NCBIN:86117, NCBIN:86118, NCBIN:86119, NCBIN:86120, NCBIN:86121, NCBIN:86122, NCBIN:86123, NCBIN:86124, NCBIN:86125, NCBIN:86126, NCBIN:86127, NCBIN:86128, NCBIN:86129, NCBIN:86130, NCBIN:86131, NCBIN:86132, NCBIN:86133, NCBIN:86134, NCBIN:86135, NCBIN:86136, NCBIN:86137, NCBIN:86138, NCBIN:86139, NCBIN:86140, NCBIN:86141, NCBIN:86142, NCBIN:86143, NCBIN:86144, NCBIN:86145, NCBIN:86146, NCBIN:86147, NCBIN:86148, NCBIN:86149, NCBIN:86150, NCBIN:86151, NCBIN:86152, NCBIN:86153, NCBIN:86154, NCBIN:86155, NCBIN:86156, NCBIN:86157, NCBIN:86158, NCBIN:86159, NCBIN:86160, NCBIN:86161, NCBIN:86162, NCBIN:86163, NCBIN:86164, NCBIN:86165, NCBIN:86166, NCBIN:86167, NCBIN:86168, NCBIN:86169, NCBIN:86170, NCBIN:86171, NCBIN:86172, NCBIN:86173, NCBIN:86174, NCBIN:86175, NCBIN:86176, NCBIN:86177, NCBIN:86178, NCBIN:86179, NCBIN:86180, NCBIN:86181, NCBIN:86182, NCBIN:86183, NCBIN:86184, NCBIN:86185, NCBIN:86186, NCBIN:86187, NCBIN:86188, NCBIN:86189, NCBIN:86190, NCBIN:86191, NCBIN:86192, NCBIN:86193, NCBIN:86194, NCBIN:86195, NCBIN:86196, NCBIN:86197, NCBIN:86198, NCBIN:86199, NCBIN:86200, NCBIN:86201, NCBIN:86202, NCBIN:86203, NCBIN:86204, NCBIN:86205, NCBIN:86206, NCBIN:86207, NCBIN:86208, NCBIN:86209, NCBIN:86210, NCBIN:86211, NCBIN:86212, NCBIN:86213, NCBIN:86214, NCBIN:86215, NCBIN:86216, NCBIN:86217, NCBIN:86218, NCBIN:86219, NCBIN:86220, NCBIN:86221, NCBIN:86222, NCBIN:86223, NCBIN:86224, NCBIN:86225, NCBIN:86226, NCBIN:86227, NCBIN:86228, NCBIN:86229, NCBIN:86230, NCBIN:86231, NCBIN:86232, NCBIN:86233, NCBIN:86234, NCBIN:86235, NCBIN:86236, NCBIN:86237, NCBIN:86238, NCBIN:86239, NCBIN:86240, NCBIN:86241, NCBIN:86242, NCBIN:86243, NCBIN:86244, NCBIN:86245, NCBIN:86246, NCBIN:86247, NCBIN:86248, NCBIN:86249, NCBIN:86250, NCBIN:86251, NCBIN:86252, NCBIN:86253, NCBIN:86254, NCBIN:86255, NCBIN:86256, NCBIN:86257, NCBIN:86258, NCBIN:86259, NCBIN:86260, NCBIN:86261, NCBIN:86262, NCBIN:86263, NCBIN:86264, NCBIN:86265, NCBIN:86266, NCBIN:86267, NCBIN:86268, NCBIN:86269, NCBIN:86270, NCBIN:86271, NCBIN:86272, NCBIN:86273, NCBIN:86274, NCBIN:86275, NCBIN:86276, NCBIN:86277, NCBIN:86278, NCBIN:86279, NCBIN:86280, NCBIN:86281, NCBIN:86282, NCBIN:86283, NCBIN:86284, NCBIN:86285, NCBIN:86286, NCBIN:86287, NCBIN:86288, NCBIN:86289, NCBIN:86290, NCBIN:86291, NCBIN:86292, NCBIN:86293, NCBIN:86294, NCBIN:86295, NCBIN:86296, NCBIN:86297, NCBIN:86298, NCBIN:86299, NCBIN:86300, NCBIN:86301, NCBIN:86302, NCBIN:86303, NCBIN:86304, NCBIN:86305, NCBIN:86306, NCBIN:86307, NCBIN:86308, NCBIN:86309, NCBIN:86310, NCBIN:86311, NCBIN:86312, NCBIN:86313, NCBIN:86314, NCBIN:86315, NCBIN:86316, NCBIN:86317, NCBIN:86318, NCBIN:86319, NCBIN:86320, NCBIN:86321, NCBIN:86322, NCBIN:86

QY 62 DSGEYKQHQVNESEPVYLEVFDWLLQASAEVVMGQPLFLRCHGRNWDVYKVIYY 121
Db 80 DSGEYKQAGGTSLSPEVLDVSDWLVLTQSLIFQEGDVLVLRCHSNWNWFLAKVTFY 139
QY 122 KGGEALKYENHNISITNATVEDSGTYCTGKWQLDYSEPLNITV 169
Db 140 HNGVAKYFISKNFSPONSHSGAYNCTGLIGRTSHTSPVITV 187
RESULT 11
JL0107
Fc gamma (IgG) receptor III-A precursor (natural killer cell) [validated] - human
N;Alternate names: CD16 antigen; low affinity IgG Fc receptor type III-2 precursor; surf
C;Species: Homo sapiens (man)
C;Date: 07-Sep-1990 #sequence revision 02-Aug-1996 #text_change 08-Dec-2000
C;Accession: J0107; A60383; A32933; I37627
R;Avatch, J.V.; Perussia, B.
J. Exp. Med. 170, 481-497, 1989
A;Title: Alternative membrane forms of Fc gamma RIII(CD16) on human natural killer cells
A;Reference number: JL0107; MUID:89328325; PMID:2526846
A;Accession: JL0107
A;Molecule type: mRNA
A;Residues: 1-254 <RAV>
A;Cross-references: GB:X52645; GB:M31937; NID:G31323; PIDN:CAA36870.1; PID:G31324
A;Note: the sequence of the receptor from human polymorphonuclear granulocytes, reported
21 residues
R;Trounstine, M.L.; Peltz, G.A.; Yssel, H.; Huizinga, T.W.J.; von dem Borne, A.E.G.K.; S
Int. Immunol. 2, 303-310, 1990
A;Title: Reactivity of cloned, expressed human Fc gamma RIII isoforms with monoclonal anti
A;Reference number: A60383; MUID:91120527; PMID:1703781
A;Accession: A60383
A;Status: not compared with conceptual translation
A;Molecule type: mRNA
A;Residues: 1-254 <TRO>
R;Scallion, B.J.; Scigliano, E.; Freedman, V.H.; Miedel, M.C.; Pan, Y.C.E.; Unkeless, J.C
Proc. Natl. Acad. Sci. U.S.A. 86, 5079-5083, 1989
A;Title: A human immunoglobulin G receptor exists in both polypeptide-anchored and phosph
A;Reference number: A32933; MUID:89236947; PMID:2525780
A;Accession: A32933
A;Molecule type: mRNA
A;Residues: 31-254 <SCA>
A;Cross-references: GB:M24853; NID:G184849; PIDN:AAA53506.1; PID:G386806
R;Gessner, J.E.; Grussemeyer, T.; Kolanus, W.; Schmidt, R.E.
J. Biol. Chem. 270, 1350-1361, 1995
A;Title: The human low affinity immunoglobulin G Fc receptor III-A and III-B genes. Mole
A;Reference number: A55439; MUID:95138131; PMID:7836402
A;Accession: I37627
A;Molecule type: DNA
A;Residues: 1-39 <RES>
A;Cross-references: EMBL:Z46222; NID:9559445; PIDN:CAA86295.1; PID:G1478198
A;Note: translation has been corrected relative to PID:G871305
C;Comment: This low affinity IgG Fc receptor of natural killer cells, which is the produ
e nearly identical, yet this receptor lacks a glycosylphosphatidylinositol anchor and in
C;Genetics:
A;Gene: GDB:FCGR3A; FCGR3
A;Cross-references: GDB:I119904; OMIM:146740
A;Map position: 1q23-1q23
A;Introns: 14/1; 21/1
A;Note: the list of introns is incomplete
C;Superfamily: Fc gamma receptor III; immunoglobulin homology
C;Keywords: glycoprotein; receptor; transmembrane protein
F;1-17/Domain: signal sequence #status predicted <SIG>
F;18-254/Product: Fc gamma (IgG) receptor III-A #status experimental <MAT>
F;18-208/Domain: extracellular #status predicted <EXT>
F;40-91/Domain: immunoglobulin homology <IMM1>
F;11-174/Domain: immunoglobulin homology <IMM2>
F;209-229/Domain: transmembrane #status predicted <TRZ>
F;230-254/Domain: intracellular #status predicted <CYT>
F;56,63,92,180,187/Binding site: carbohydrate (Asn) (covalent) #status predicted

Query Match 38.1%; Score 361; DB 1; Length 254;
Best Local Similarity 44.0%; Pred. NO. 3.1e-22;

Matches 73; Conservative 26; Mismatches 67; Indels 0; Gaps 0;
QY 4 KPKVSLNPPNRIKFGENVTLTCGNPNFFVSTKTFHNGSLSEETNSLINVNAKPEDS 63
Db 25 KAVVLEPQRYVLEKDSVTLKCGAYSPEDNSTQWPHNESLSSQASSYFIDAATVDDS 84
QY 64 GEYKQHQVNESEPVYLEVFDWLLQASAEVVMGQPLFLRCHGRNWDVYKVIYYKD 123
Db 85 GEYKQNLSTLSDFVQLEHVHIGWLLQAPRWVKEEDPHLRCHSKWNTALHKVTLQON 144
QY 124 GEALKYENHNISITNATVEDSGTYCTGKWQLDYSEPLNITV 169
Db 145 KGGRKYFHNSDFYIPKATLKDSGYFCRGLFGKNVSETVAITI 190

RESULT 12

S36903
Fc gamma (IgG) receptor type 2 precursor - rat
C;Species: Rattus norvegicus (Norway rat)
C;Date: 22-Jan-1994 #sequence_revision 10-Nov-1995 #text_change 23-Jul-1999
C;Accession: S36903
R;Boseck, P.; Pecht, I.
FEBS Lett. 331, 86-90, 1993
A;Title: Cloning and sequence of the cDNA coding for rat type II Fc-gamma receptor of ma
A;Reference number: S36903; MUID:94009652; PMID:8405417
A;Accession: S36903
A;Molecule type: mRNA
A;Residues: 1-285 <BOC>
A;Cross-references: EMBL:X73371; NID:G37576; PIDN:CAA51788.1; PID:G397577
C;Superfamily: Fc gamma receptor III; immunoglobulin homology
C;Keywords: immunoglobulin receptor
F;52-103/Domain: immunoglobulin homology <IMM>

Query Match 37.8%; Score 358; DB 2; Length 285;
Best Local Similarity 40.4%; Pred. NO. 6.3e-22;

Matches 67; Conservative 33; Mismatches 66; Indels 0; Gaps 0;
QY 4 KPKVSLNPPNRIKFGENVTLTCGNPNFFVSTKTFHNGSLSEETNSLINVNAKPEDS 63
Db 37 KAVVLEPQRYVLEKDSVTLKCGAYSPEDNSTQWPHNESLSSQASSYFIDAATVDDS 96
QY 64 GEYKQHQVNESEPVYLEVFDWLLQASAEVVMGQPLFLRCHGRNWDVYKVIYYKD 123
Db 97 GEYKQNLSTLSDFVQLEHVHIGWLLQAPRWVKEEDPHLRCHSKWNTALHKVTLQON 156
QY 124 GEALKYENHNISITNATVEDSGTYCTGKWQLDYSEPLNITV 169
Db 157 GKPVYHYHQSNNFSPKANSHSGNYCKAYLGRTHMYSKPTITV 202

RESULT 13

JU0284
Fc gamma (IgG) receptor III-B precursor (neutrophil) - human
N;Alternate names: FcR III; IgG Fc receptor precursor, type III-1 (polymorphonuclear gra
C;Species: Homo sapiens (man)
C;Date: 07-Sep-1990 #sequence_revision 02-Aug-1996 #text_change 28-Jan-2000
C;Accession: JU0284; S00758; I37628; B32933; A31460
R;Avatch, J.V.; Perussia, B.
J. Exp. Med. 170, 481-497, 1989
A;Title: Alternative membrane forms of Fc gamma RIII(CD16) on human natural killer cells
A;Reference number: JL0107; MUID:89328325; PMID:2526846
A;Accession: JU0284
A;Molecule type: mRNA
A;Residues: 1-201, 204-233 <RAV>
A;Cross-references: GB:J04162
A;Note: the sequence of the receptor from human NK cells, reported in the same paper, d
rboxyl end
R;Simmons, D.; Seed, B.
Nature 333, 568-570, 1988
A;Title: The Fc-gamma receptor of natural killer cells is a phospholipid-linked membrane
A;Reference number: S00758; MUID:89232937; PMID:2967436
A;Accession: S00758
A;Molecule type: mRNA

A;Residues: 1-233 <SIM>
A;Cross-references: EMBL:X07934; NID:G29744; PIDN:CAA30758.1; PID:G29745
R;Gessner, J.E.; Grussemeyer, T.; Kolanus, W.; Schmidt, R.E.
J. Biol. Chem. 270, 1350-1361, 1995
A;Title: The human low affinity immunoglobulin G Fc receptor III-A and III-B genes. Mole
A;Reference number: A55439; MUID:95138131; PMID:7836402
A;Accession: I37628
A;Molecule type: DNA
A;Residues: 1-72 <RES>
A;Cross-references: EMBL:Z46223; NID:G559446; PIDN:CAA86296.1; PID:9871306
R;Scallan, B.J.; Scigliano, E.; Freedman, V.H.; Miedel, M.C.; Pan, Y.C.E.; Unkeless, J.C.
Proc. Natl. Acad. Sci. U.S.A. 86, 5079-5083, 1989
A;Title: A human immunoglobulin G receptor exists in both polypeptide-anchored and phos
A;Reference number: A32933; MUID:8926947; PMID:2525780
A;Accession: B32933
A;Molecule type: mRNA
A;Residues: 1-121, 'E', 123-150, 'S', 152-233 <SCA>
A;Cross-references: GB:M24854; NID:G184851; PIDN:AAA3507.1; PID:G306930
R;Peltz, G.A.; Grundy, H.O.; Lebo, R.V.; Yssel, H.; Barsh, G.S.; Moore, K.W.
Proc. Natl. Acad. Sci. U.S.A. 86, 1013-1017, 1989
A;Title: Human Fc-gamma-RIII: cloning, expression, and identification of the chromosomal
A;Reference number: A31460; MUID:89128838; PMID:2521732
A;Accession: A31460
A;Molecule type: mRNA
A;Residues: 1-35, 'R', 37-64, 'N', 66-81, 'D', 83-105, 'V', 107-233 <PEL>
A;Cross-references: GB:J04162; NID:G183036; PIDN:AAA35881.1; PID:G183037
C;Comment: This low affinity IGG Fc receptor of neutrophils, which is the product of the
I, yet this receptor lacks 21 residues at the carboxyl end because of an early stop cod
C;Genetics:
A;Gene: GDB:FCGR3B; FCGR3
A;Cross-references: GDB:128176; OMIM:146740
A;Map position: 1q23-1q23
A;Introns: 14/1; 21/1
A;Note: the list of introns is incomplete
C;Superfamily: Fc gamma receptor III; immunoglobulin homology
C;Keywords: blocked carboxyl end; glycoprotein; lipoprotein; phosphatidylinositol linkag
F;1-18/Domain: signal sequence #status predicted <SIG>
F;19-203/Product: Fc gamma (IgG) receptor III-B #status predicted <MAT>
F;40-91/Domain: immunoglobulin homology <IMM1>
F;111-174/Domain: immunoglobulin homology <IMM2>
F;56,63,82,92,180,187/Binding site: carbohydate (Asn) (covalent) #status predicted
F;203/Modified site: GPI-anchor ethanolamine amidated carboxyl end (Ser) (in mature form

Query Match 37.7%; Score 357; DB 1; Length 233;
Best Local Similarity 44.0%; Pred. No. 6e-22;
Matches 73; Conservative 25; Mismatches 68; Indels 0; Gaps 0;
QY 4 KPVSLNPPNRRIFKGENVTITCNNGNFFVSSSTKFWHSLSEETNSSLINIVNAKPEDS 63
DB 25 KAVVLEFPQVSVLEKDSVTLKCGAGVSPEDNSTOWPHNESLSSQASSYFIDAATVND 84
QY 64 GEYKCOHQVNEBPVYLVFSDWLLLOQSAEVVMEQPLFLCHGWRNDVYKVIYKD 123
DB 85 GEYFCQNLSTLSDPQVLEHIGLLLOQAPRWVFKEDPDLHCHSKNTALHKVLYQN 144
QY 124 GEALKYWEHNHISITNATVEDSGTYCTGKWQDYSEPLNITY 169
DB 145 GKDRKYFHNSDFHPRATLKDGSYFCRGLVGSKNVSETVNI 190

RESULT 14
FCMSG1
Fc gamma (IgG) receptor II (low affinity) beta (splice form 2) precursor - mouse
N;Alternate names: macrophage-lymphocyte IgG1/IgG2b Fc receptor
C;Species: Mus musculus (house mouse)
C;Date: 31-Dec-1989 #sequence_revision 16-Aug-1996 #text change 10-Sep-1999
C;Accession: B40071; S29362; A93384; A94125; A25741; A25901
R;Hogarth, P.M.; Witort, E.; Hulett, M.D.; Bonnerot, C.; Even, J.; Fridman, W.H.; McKenz
J. Immunol. 146, 369-376, 1991
A;Title: Structure of the mouse beta2fcgamma receptor II gene.
A;Reference number: A40071; MUID:91079576; PMID:1824594
A;Accession: B40071
A;Status: preliminary

A;Molecule type: DNA
A;Residues: 1-283 <HOG>
R;Ravech, J.V.; Luster, A.D.; Weinshank, R.; Kochan, J.; Pavlovic, A.; Portnoy, D.A.; H
Science 234, 718-725, 1986
A;Title: Structural heterogeneity and functional domains of murine immunoglobulin G Fc r
A;Reference number: S29360; MUID:87042761; PMID:2946078
A;Accession: S29362
A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-283 <RAV>
A;Cross-references: EMBL:W14216; NID:G193258; PIDN:AAA37609.1; PID:G309231
R;Lewis, V.A.; Koch, T.; Plutner, H.; Wellman, I.
Nature 324, 372-375, 1986
A;Title: A complementary DNA clone for a macrophage-lymphocyte Fc receptor.
A;Reference number: A93384; MUID:87065089; PMID:3024012
A;Accession: A93384
A;Molecule type: mRNA
A;Residues: 17-283 <LEW>
R;Hibbs, M.L.; Walker, I.D.; Kirsztbaum, L.; Pietersz, G.A.; Deacon, N.J.; Chambers, G.W.
Proc. Natl. Acad. Sci. U.S.A. 83, 6980-6984, 1986
A;Title: The murine Fc receptor for immunoglobulin: purification, partial amino acid seq
A;Reference number: A94125; MUID:86313694; PMID:2944118
A;Accession: A94125
A;Molecule type: mRNA
A;Residues: 17-45;255-277 <HIB>
A;Note: parts of this sequence, including the amino end of the mature protein, were dete
C;Genetics:
A;Map position: 1
C;Superfamily: Fc gamma receptor III; immunoglobulin homology
C;Keywords: alternative splicing; duplication; glycoprotein; immunoglobulin receptor; tr
F;1-23/Domain: signal sequence #status predicted <SIG>
F;30-283/Product: Fc gamma receptor II beta, form 2 #status predicted <MAT>
F;50-101/Domain: immunoglobulin homology <IMM1>
F;131-184/Domain: immunoglobulin homology <IMM2>
F;209-236/Domain: transmembrane #status predicted <TM>
F;237-283/Domain: intracellular #status predicted <INT>
F;57-99,138-182/Disulfide bonds: #status predicted
F;65,92,166,173/Binding site: carbohydate (Asn) (covalent) #status predicted

Query Match 37.4%; Score 354; DB 1; Length 283;
Best Local Similarity 41.9%; Pred. No. 1.3e-21;
Matches 70; Conservative 32; Mismatches 63; Indels 2; Gaps 2;
QY 4 KPVSLNPPNRRIFKGENVTITCNNGNFFVSSSTKFWHSLSEETNSSLINIVNAKPED 62
DB 35 KAVVLEFPQVSVLEKDSVTLKCGAGVSPEDNSTOWPHNESLSSQASSYFIDAATVND 93
QY 63 SGEYKCOHQVNEBPVYLVFSDWLLLOQSAEVVMEQPLFLCHGWRNDVYKVIYK 122
DB 94 SGEYFCQNEQFLSDPQVLEHIGLLLOQAPRWVFKEDPDLHCHSKNTALHKVLYQN 153
QY 123 DEALKYWEHNHISITNATVEDSGTYCTGKWQDYSEPLNITY 169
DB 154 NEKSVRYHHYSSNFSIPKANHSHSGDYCKGSLGRTLHQSXPVTITY 200

RESULT 15
A40071
Fc gamma (IgG) receptor II (low affinity) beta (splice form 1) precursor - mouse
C;Species: Mus musculus (house mouse)
C;Date: 06-Mar-1992 #sequence_revision 06-Mar-1992 #text change 23-Jul-1999
C;Accession: A40071; A60761; S29361
R;Hogarth, P.M.; Witort, E.; Hulett, M.D.; Bonnerot, C.; Even, J.; Fridman, W.H.; McKenz
J. Immunol. 146, 369-376, 1991
A;Title: Structure of the mouse beta2fcgamma receptor II gene.
A;Reference number: A40071; MUID:91079576; PMID:1824594
A;Accession: A40071
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-330 <HOG>
A;Cross-references: GB:M63284; NID:G192161; PIDN:AAA37289.1; PID:G192163
R;Lah, M.; Quelch, K.; Deacon, N.J.; McKenzie, I.F.C.; Hogarth, P.M.
Immunogenetics 31, 202-206, 1990

```

A:Title: Identification of the mouse beta Fc gammaRII polymorphism by direct sequencing c
A:Reference number: A60761; MUID:90202030; PMID:2138587
A:Accession: A60761
A>Status: preliminary; nucleic acid sequence not shown; translation not shown
A:Molecule type: mRNA
A:Residues: 1-144, 'P', 146-189, 'Q', 191-298, 'P', 300-330 <LAH>
A:Cross-references: GB:IM31312; MID:G1932260; PIDN:AAA37610.1; PID:G397155
R:Ravetch, J.V.; Luster, A.D.; Weinshank, R.; Kocan, J.; Pavlovic, A.; Portnoy, D.A.; H
Science 234, 718-725, 1986
A:Title: Structural heterogeneity and functional domains of murine immunoglobulin G Fc R
A:Reference number: S29360; MUID:87042761; PMID:2946078
A:Accession: S29361
A>Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-269, 'L', 271, 'A', 'C', 276, 'R', 279-330 <RAV>
A:Cross-references: EMBL:M16367; NID:G193256; PIDN:AAA37608.1; PID:G309230
C:Superfamily: Fc gamma receptor III; immunoglobulin homology
C:Keywords: immunoglobulin receptor
F:1-29/Domain: signal sequence #status predicted <SIG>
F:50-101/Domain: immunoglobulin homology <IMM1>
F:131-184/Domain: immunoglobulin homology <IMM2>

Query Match 37.4%; Score 354; DB 2; Length 330;
Best Local Similarity 41.9%; Pred. No. 1.6e-21;
Matches 70; Conservative 32; Mismatches 63; Indels 2; Gaps 2;

QY 4 KPKVSLNPWNRIKGNENTLTCNGNPFVSTKWFHNG-SLSBETNSLSNIVAKED 62
Db 35 KAVVLEPPWIKVQKEDTTLTCGTHNFGNSITQWFGNSIRSQVQASYTF-KATVND 93
QY 63 SGGYKCHQCHQWNESEFPVILEFSDMLLQASAEVNVNGOPFLIRCHGMENWVDYKVIYK 122
Db 94 SGYRQMEQTRLSDFVDLCVISDWLLLTQPOLVFLFEGETITILRCHSWKNLLNRISSPH 153
QY 123 DGEALXYWENHNISITNATVEDSGYITGKVKWQLDYESEPLNIV 169
Db 154 NEKSVRYHYHNSFIPKANHSBGDYKGSIGLRTLHQS KPVITV 200

Search completed: October 6, 2004, 09:23:44
Job time : 10.4219 secs

```

This Page Blank (uspto)

GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.

OM protein - protein search, using sw model

Run on: October 6, 2004, 08:59:39 ; Search time 5.81352 Seconds
(without alignments)
1540.558 Million cell updates/sec

Title: US-10-763-400-13

Perfect score: 947
Sequence: 1 VFQPKVSLNPPNRFKGE.....GKWLQDYSEPLNITVIKA 172

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 141681 seqs, 52070155 residues

Total number of hits satisfying chosen parameters: 141681

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : SwissProt_42.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	947	100.0	257	1 FCEA_HUMAN	P12319 homo sapien
2	472	49.8	250	1 FCEA_MOUSE	P20489 mus musculus
3	468	49.4	245	1 FCE1_RAT	P12371 rattus norv
4	381	40.2	296	1 FCG2_BOVIN	Q28110 bos taurus
5	374.5	39.5	374	1 FCG1_HUMAN	P12314 homo sapien
6	369	39.0	404	1 FCG1_MOUSE	P26151 mus musculus
7	365	38.5	250	1 FCG3_BOVIN	P79107 bos taurus
8	363	38.3	341	1 FCG2_CAVPO	Q60513 cavia porce
9	361	38.1	254	1 FCG3_HUMAN	P08637 homo sapien
10	360	38.0	257	1 FCG3_PIG	Q28942 sus scrofa
11	358	37.8	285	1 FCG2_RAT	Q63203 rattus norv
12	357	37.7	233	1 FCG3_HUMAN	O75015 homo sapien
13	354	37.4	330	1 FCG2_MOUSE	P08101 mus musculus
14	353	37.3	267	1 FCG3_RAT	P27645 rattus norv
15	352	37.2	261	1 FCG3_MOUSE	P08508 mus musculus
16	339	35.8	316	1 FCGA_PANTR	Q8SPV8 pan troglod
17	335	35.4	310	1 FCG3_HUMAN	P31994 homo sapien
18	335	35.4	323	1 FCGC_HUMAN	P11995 homo sapien
19	328	34.6	317	1 FCGA_HUMAN	P12318 homo sapien
20	327	34.5	157	1 FCE2_RAT	P12840 rattus norv
21	166.5	17.6	1709	1 SN_HUMAN	Q5B222 homo sapien
22	161	17.0	1694	1 SN_MOUSE	Q62230 mus musculus
23	152	16.1	422	1 K3L1_RAT	P83556 rattus norv
24	144	15.2	432	1 K3L1_MOUSE	P83556 mus musculus
25	136.5	14.4	521	1 CEA1_MOUSE	P31809 mus musculus
26	133.5	14.1	837	1 NCM2_MOUSE	Q35136 mus musculus
27	130	13.7	519	1 ECTO_RAT	P16573 rattus norv
28	128.5	13.6	344	1 CEA1_HUMAN	P40199 homo sapien
29	126.5	13.4	1302	1 NRG_DROME	P20241 crosophila
30	120	12.7	6632	1 UN89_CABEL	O01761 caenorhabdi
31	117	12.4	1197	1 CAM1_BRARE	Q90478 brachydanio
32	116.5	12.3	978	1 KFW5_RAT	Q00495 rattus norv
33	116	12.2	1240	1 NFAS_HUMAN	O94856 homo sapien

ALIGNMENTS

RESULT 1

ID	FCFA_HUMAN	STANDARD;	PRT;	257 AA.
AC	P12319			
DT	01-OCT-1989 (Rel. 12, Created)			
DT	01-OCT-1989 (Rel. 12, Last sequence update)			
DT	10-OCT-2003 (Rel. 42, Last annotation update)			
DE	High affinity immunoglobulin epsilon receptor alpha-subunit precursor (FCERI) (Ige Fc receptor, alpha-subunit) (Fc-epsilon RI-alpha).			
GN	FCERI1 OR FCE1A.			
OS	Homo sapiens (Human).			
OC	Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;			
OC	Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.			
OX	NCBI_TaxID=9606;			
RN	[1]			
RP	SEQUENCE FROM N.A.			
RX	MEDLINE=88233953; PubMed=2967464;			
RA	Kochan J., Pettine L.F., Hakimi J., Kishi K., Kinet J.-P.;			
RT	"Isolation of the gene coding for the alpha subunit of the human high affinity Ige receptor.";			
RT	Nucleic Acids Res. 16:3584-3584(1988).			
RL	[2]			
RP	SEQUENCE FROM N.A., AND PARTIAL SEQUENCE.			
RC	TISSUE=Mast cells;			
RX	MEDLINE=88158102; PubMed=2964640;			
RA	Shimizu A., Tepler J., Benfey P.N., Berenstein E.H., Siraganian R.P., Leder P.;			
RT	"Human and rat mast cell high-affinity immunoglobulin E receptors: characterization of putative alpha-chain gene products.";			
RL	[3]			
RP	Proc. Natl. Acad. Sci. U.S.A. 85:1907-1911(1988).			
RN	[3]			
RP	3D-STRUCTURE MODELING OF 26-197			
RX	MEDLINE=93113350; PubMed=1472946;			
RA	Padlan E.A., Helm B.A.;			
RT	"A modeling study of the alpha-subunit of human high-affinity receptor for immunoglobulin-E.";			
RL	Receptor 2:129-144(1992).			
CC	-!- FUNCTION: BINDS TO THE FC REGION OF IMMUNOGLOBULINS EPSILON. HIGH AFFINITY RECEPTOR. RESPONSIBLE FOR INITIATING THE ALLERGIC RESPONSE. BINDING OF ALLERGEN TO RECEPTOR-BOUND IGE LEADS TO CELL ACTIVATION AND THE RELEASE OF MEDIATORS (SUCH AS HISTAMINE) RESPONSIBLE FOR THE MANIFESTATIONS OF ALLERGY. THE SAME RECEPTOR . ALSO INDUCES THE SECRETION OF IMPORTANT LYMPHOKINES.			
CC	-!- SUBUNIT: TETRAMER OF AN ALPHA CHAIN, A BETA CHAIN, AND TWO DISULFIDE LINKED GAMMA CHAINS.			
CC	-!- SUBCELLULAR LOCATION: Type 1 membrane protein.			
CC	-!- SIMILARITY: Contains 2 immunoglobulin-like domains.			
CC	-----			
CC	This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation - the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/ or send an email to license@isb-sib.ch).			
CC	-----			

Q05793 mus musculus
P20273 homo sapien
P09581 mus musculus
P06731 homo sapien
Q15394 homo sapien
Q63198 rattus norv
Q81003 mus musculus
P97685 rattus norv
Q12860 homo sapien
P12960 mus musculus
P35329 mus musculus
Q08340 macaca neme

DR EMBL; X06948; CAA30025.1; -;
 DR EMBL; J03605; AAA36204.1; -;
 DR EMBL; A21606; CAA01564.1; -;
 DR PIR; S00682; S00682;
 DR PDB; IALS; 27-FEB-95.
 DR PDB; IALT; 27-FEB-95.
 DR PDB; 1P2Q; 08-JUN-00.
 DR PDB; 1J86; 29-AUG-01.
 DR PDB; 1J87; 29-AUG-01.
 DR PDB; 1J88; 29-AUG-01.
 DR PDB; 1J89; 05-SEP-01.
 DR PDB; 1J89; 05-SEP-01.
 DR Genew; HGNC:3609; FCER1A.
 DR MIM; 147140; -;
 DR GO; GO:0005887; C:integral to plasma membrane; TAS.
 DR InterPro; IPR007110; IG-like.
 DR InterPro; IPR003598; IG_c2.
 DR Pfam; PF00047; Ig; 2.
 DR SMART; SM00408; IGC2; 1.
 DR PROSITE; PS50835; IG-LIKE; 2.
 DR IGE-binding protein; Receptor; Transmembrane; Glycoprotein; Signal;
 KW Immunoglobulin domain; Repeat; 3D-structure.
 FT SIGNAL 1 25
 FT CHAIN 26 257
 FT DOMAIN 26 205
 FT TRANSMEM 206 224
 FT DOMAIN 225 257
 FT DOMAIN 30 110
 FT DOMAIN 111 193
 FT DISULFID 51 93
 FT DISULFID 132 176
 FT CARBOHYD 46 46
 FT CARBOHYD 67 67
 FT CARBOHYD 75 75
 FT CARBOHYD 99 99
 FT CARBOHYD 160 160
 FT CARBOHYD 165 165
 FT CARBOHYD 191 191
 FT STRAND 31 35
 FT HELIX 39 43
 FT TURN 43 43
 FT STRAND 48 54
 FT STRAND 61 66
 FT TURN 67 68
 FT STRAND 69 71
 FT STRAND 74 74
 FT TURN 75 76
 FT STRAND 77 79
 FT STRAND 82 87
 FT HELIX 91 96
 FT TURN 98 100
 FT TURN 101 101
 FT STRAND 104 107
 FT STRAND 114 116
 FT HELIX 120 124
 FT STRAND 128 133
 FT STRAND 143 145
 FT STRAND 146 148
 FT TURN 149 149
 FT STRAND 150 150
 FT TURN 152 153
 FT STRAND 154 155
 FT TURN 156 159
 FT STRAND 160 163
 FT HELIX 165 170
 FT STRAND 175 178
 FT STRAND 181 182
 FT TURN 183 185
 FT STRAND 186 187
 FT STRAND 190 193
 SQ SEQUENCE 257 AA; 29596 MW; F183BB2357DDAD58 CRC64;
 Query Match 100.0%; Score 947; DB 1; Length 257;

Best Local Similarity 100.0%; Pred. No. 5,8e-77;
 Matches 172; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 VPQKPKVSLNPPNRIKFGENTVLTICNGNNPFVSTKWFHNGSLSEETNSLNIIVNAKF 60
 DB 26 VPQKPKVSLNPPNRIKFGENTVLTICNGNNPFVSTKWFHNGSLSEETNSLNIIVNAKF 85
 QY 61 EDSEYKCOHQQWSESEPVYLFVSDMLLQSAEVMWEGQLFLRCHGRWMDYKVIY 120
 DB 86 EDSEYKCOHQQWSESEPVYLFVSDMLLQSAEVMWEGQLFLRCHGRWMDYKVIY 145
 QY 121 YKDGALKYWNHNSITNATVEDSGTYCTGKVMQLDYSEPLNITVIKA 172
 DB 146 YKDGALKYWNHNSITNATVEDSGTYCTGKVMQLDYSEPLNITVIKA 197
 RESULT 2
 FCEA_MOUSE
 ID FCEA_MOUSE STANDARD; PRT; 250 AA.
 AC P20489;
 DT 01-FEB-1991 (Rel. 17, Created)
 DT 01-FEB-1991 (Rel. 17, Last sequence update)
 DT 10-OCT-2003 (Rel. 42, Last annotation update)
 DE High affinity immunoglobulin epsilon receptor alpha-subunit precursor
 DE (FCERI) (IGE FC receptor, alpha-subunit) (FC-epsilon RI-alpha).
 GN FCERIA OR FCEIA.
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 OX NCBI_TaxID=10090;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=89359361; PubMed=2527850;
 RA Ra C., Jouvin M.H.E., Kinet J.-P.;
 RT "Complete structure of the mouse mast cell receptor for IgE (Fc
 epsilon RI) and surface expression of chimeric receptors
 (rat-mouse-human) on transfected cells.";
 RL J. Biol. Chem. 264:15323-15327(1989).
 CC -!- FUNCTION: BINDS TO THE FC REGION OF IMMUNOGLOBULIN EPSILON. HIGH
 CC AFFINITY RECEPTOR. RESPONSIBLE FOR INITIATING THE ALLERGIC
 CC RESPONSE. BINDING OF ALLERGEN TO RECEPTOR-BOUND IGE LEADS TO CELL
 CC ACTIVATION AND THE RELEASE OF MEDIATORS (SUCH AS HISTAMINE)
 CC RESPONSIBLE FOR THE MANIFESTATIONS OF ALLERGY. THE SAME RECEPTOR
 CC ALSO INDUCES THE SECRETION OF IMPORTANT LYMPHOKINES.
 CC -!- SUBUNIT: TETRAMER OF AN ALPHA CHAIN, A BETA CHAIN, AND TWO
 CC DISULFIDE LINKED GAMMA CHAINS.
 CC -!- SUBCELLULAR LOCATION: Type 1 membrane protein.
 CC -!- SIMILARITY: Contains 2 immunoglobulin-like domains.
 CC
 CC This SWISS-PROT entry is copyright. It is produced through a collaboration
 CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
 CC the European Bioinformatics Institute. There are no restrictions on its
 CC use by non-profit institutions as long as its content is in no way
 CC modified and this statement is not removed. Usage by and for commercial
 CC entities requires a license agreement (See <http://www.isb-sib.ch/announce/>
 CC or send an email to license@isb-sib.ch).
 CC
 CC EMBL; J05018; AAA37600.1; -;
 CC FIR; A34342; A34342.
 CC HSP; P12319; IALS.
 CC MGI; 95494; Fcer1a.
 CC GO; GO:0007165; P:signal transduction; IDA.
 CC InterPro; IPR007110; IG-like.
 CC InterPro; IPR003599; IG.
 CC Pfam; PF00047; Ig; 2.
 CC SMART; SM00409; IG; 2.
 CC PROSITE; PS50835; IG-LIKE; 1.
 KW IGE-binding protein; Receptor; Transmembrane; Glycoprotein; Signal;
 KW Immunoglobulin domain; Repeat.
 FT SIGNAL 1 23
 FT CHAIN 24 250
 FT DOMAIN 24 204
 FT HIGH AFFINITY IMMUNOGLOBULIN EPSILON
 FT RECEPTOR ALPHA-SUBUNIT.
 FT EXTRACELLULAR (POTENTIAL).
 FT

```

FT TRANSMEM 205 223 POTENTIAL.
FT DOMAIN 224 250 CYTOPLASMIC (POTENTIAL).
FT DOMAIN 28 104 IG-LIKE 1.
FT DOMAIN 114 181 IG-LIKE 2.
FT DISULFID 49 92 BY SIMILARITY.
FT DISULFID 131 174 BY SIMILARITY.
FT CARBOHYD 58 58 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 66 66 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 73 73 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 106 106 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 152 152 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 167 167 N-LINKED (GLCNAC. .) (POTENTIAL).
SQ SEQUENCE 250 AA; 28672 MW; 2575D1BF84DC0C4E CRC64;

Query Match 49.8%; Score 472; DB 1; Length 250;
Best Local Similarity 51.5%; Pred. No. 7.4e-35;
Matches 88; Conservative 35; Mismatches 46; Indels 2; Gaps 2;

QY 3 QPKVSLNPPNRIKGVNTLTCNGNNFFEV-SSTKWFHNGSLSEETNSLNIIVNAKFE 61
DB 26 EKSVTLDPFWIRIFTGKVLSCYCNHNLQNSITKWIHNGTVSEVNSHLVIVSATVQ 85

QY 62 DSGEYKCOHQVNESEPVYLFVSDWLLQLQASAEVMEGQPLFLRCHGWRNWDVYKVIYY 121
DB 86 DSGYICQKQGLFKSKPVYLVNTQDWLLQLQTSADMILVHGSFDIRCHGWRNWDVYKVIYY 145

QY 122 KDGEALKYWEYHNHNSITNAVDSGTYYCTGKVAQLDYSEPLNITVIKA 172
DB 146 RNDHAFNYSYES-PVSIREATLNDSGTVHCKGYLRQVEYSDFKRIAVVKA 195

RESULT 3
FCBL RAT STANDARD; PRT; 245 AA.
AC P12371,
DT 01-OCT-1989 (Rel. 12, Created)
DT 01-OCT-1989 (Rel. 12, Last sequence update)
DE 10-OCT-2003 (Rel. 42, Last annotation update)
DE High affinity immunoglobulin epsilon receptor alpha-subunit precursor
DE (FCERI) (IGE FC receptor, alpha-subunit) (FC-epsilon RI-alpha).
GN FCERIA OR FCEIA.
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Eutelestomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX NCBI_TaxID=10116;
RN [1]
RN SEQUENCE FROM N.A.
RX MEDLINE=88024987; PubMed=2959318;
RA Kinet J.-P., Metzger H., Hakini J., Kochan J.;
RT "A cDNA presumptively coding for the alpha subunit of the receptor.
RT with high affinity for immunoglobulin E.";
RL Biochemistry 26:4605-4610(1987).
RN [2]
RN REVISIONS.
RA Kochan J.;
RL Submitted (MAR-1988) to the EMBL/GenBank/DBJ databases.
RN [3]
RN SEQUENCE FROM N.A.
RC TISSUE=Mast cells;
RX MEDLINE=86158102; PubMed=2964640;
RA Shimizu A., Tepler I., Benfey P.N., Berenstein E.H., Siraganian R.P.,
RA Leder P.;
RT "Human and rat mast cell high-affinity immunoglobulin E receptors:
RT characterization of putative alpha-chain gene products.";
RL Proc. Natl. Acad. Sci. U.S.A. 85:1907-1911(1988).
RN [4]
RN SEQUENCE OP 21-245 FROM N.A.
RX MEDLINE=86289772; PubMed=2969594;
RA Liu F.-T., Albrandt K., Robertson M.W.;
RT "cDNA heterogeneity suggests structural variants related to the high-
RT affinity IGE receptor.";
RL Proc. Natl. Acad. Sci. U.S.A. 85:5639-5643(1988).
CC -!- FUNCTION: BINDS TO THE FC REGION OF IMMUNOGLOBULINS EPSILON. HIGH

```

```

CC AFFINITY RECEPTOR. RESPONSIBLE FOR INITIATING THE ALLERGIC
CC RESPONSE. BINDING OF ALLERGEN TO RECEPTOR-BOUND IGE LEADS TO CELL
CC ACTIVATION AND THE RELEASE OF MEDIATORS (SUCH AS HISTAMINE)
CC RESPONSIBLE FOR THE MANIFESTATIONS OF ALLERGY. THE SAME RECEPTOR
CC ALSO INDUCES THE SECRETION OF IMPORTANT LYMPHOKINES.
CC -!- SUBUNIT: TETRAMER OF AN ALPHA CHAIN, A BETA CHAIN, AND TWO
CC DISULFIDE LINKED GAMMA CHAINS.
CC -!- SUBCELLULAR LOCATION: Type 1 membrane protein.
CC -!- SIMILARITY: Contains 2 immunoglobulin-like domains.
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use by non-profit institutions as long as its content is in no way
CC modified and this statement is not removed. Usage by and for commercial
CC entities requires a license agreement (See http://www.isb-sib.ch/
CC or send an email to license@isb-sib.ch).
CC -----
CC EMBL; M17153; AAA42045.1; -;
CC EMBL; J03606; AAA41582.1; -;
CC EMBL; M21622; AAA41146.1; -;
CC PIR; C31327; A30154.
CC HSSP; P12319; IALS.
CC InterPro; IPR007110; IG-Like.
CC InterPro; IPR003599; IG.
CC Pfam; P200047; ig; 2.
CC SMART; SM00409; IG; 2.
CC PROSITE; PS50835; IG LIKE; 1.
CC IGE-binding protein; Receptor; Transmembrane; Glycoprotein; Signal;
CC Immunoglobulin domain; Repeat.
CC SIGNAL 1 23
CC CHAIN 24 245 HIGH AFFINITY IMMUNOGLOBULIN EPSILON
CC RECEPTOR ALPHA-SUBUNIT.
CC EXTRACELLULAR (POTENTIAL).
CC POTENTIAL.
CC CYTOPLASMIC (POTENTIAL).
CC IG-LIKE 1.
CC IG-LIKE 2.
CC BY SIMILARITY.
CC N-LINKED (GLCNAC. .) (POTENTIAL).
CC N-LINKED (GLCNAC. .) (POTENTIAL).
CC N-LINKED (GLCNAC. .) (POTENTIAL).
CC N-LINKED (GLCNAC. .) (POTENTIAL).
CC N-LINKED (GLCNAC. .) (POTENTIAL).
CC N-LINKED (GLCNAC. .) (POTENTIAL).
CC N-LINKED (GLCNAC. .) (POTENTIAL).
CC SEQUENCE 245 AA; 27793 MW; A0B67DD363B72197 CRC64;

Query Match 49.4%; Score 468; DB 1; Length 245;
Best Local Similarity 50.9%; Pred. No. 1.6e-34;
Matches 86; Conservative 33; Mismatches 50; Indels 0; Gaps 0;

QY 3 QPKVSLNPPNRIKGVNTLTCNGNNFFEVSTKWFHNGSLSEETNSLNIIVNAKFE 62
DB 26 QKSVVSLDPPWIRILTGTGKVLTCNGNNSQNMSTKWIHNDISNVKSHWIVSATIQD 85

QY 63 SGGEYKCOHQVNESEPVYLFVSDWLLQLQASAEVMEGQPLFLRCHGWRNWDVYKVIYY 122
DB 86 SGYICQKQGLFKSKPVYLVNTQDWLLQLQTSADMILVHGSFDIRCHGWRNWDVYKVIYY 145

QY 123 DGEALKYWEYHNHNSITNAVDSGTYYCTGKVAQLDYSEPLNITVIK 171
DB 146 DDIAFKYSYDSNNISIRKATFNDSGSHCTGYLNKVECKSKDFSIKAVK 194

RESULT 4
FCG2_BOVIN
ID FCG2_BOVIN STANDARD; PRT; 296 AA.
AC Q28110;
DT 01-NOV-1997 (Rel. 35, Created)
DT 01-NOV-1997 (Rel. 35, Last sequence update)
DT 10-OCT-2003 (Rel. 42, Last annotation update)

```



```

KW Immunoglobulin domain; Repeat; Alternative splicing; Polymorphism.
FT SIGNAL 1 21
FT CHAIN 22 374
FT
FT HIGH AFFINITY IMMUNOGLOBULIN GAMMA FC
FT
FT RECEPTOR I.
FT EXTRACELLULAR (POTENTIAL).
FT POTENTIAL.
FT CYTOPLASMIC (POTENTIAL).
FT IG-LIKE C2-TYPE 1.
FT IG-LIKE C2-TYPE 2.
FT IG-LIKE C2-TYPE 3.
FT BY SIMILARITY.
FT BY SIMILARITY.
FT BY SIMILARITY.
FT N-LINKED (GLCNAC. .) (POTENTIAL).
FT N-LINKED (GLCNAC. .) (POTENTIAL).
FT N-LINKED (GLCNAC. .) (POTENTIAL).
FT N-LINKED (GLCNAC. .) (POTENTIAL).
FT N-LINKED (GLCNAC. .) (POTENTIAL).
FT N-LINKED (GLCNAC. .) (POTENTIAL).
FT N-LINKED (GLCNAC. .) (POTENTIAL).
FT N-LINKED (GLCNAC. .) (POTENTIAL).
FT HEKVTSSIQEDRHLEELKQEQEEQOEGVHRKEPOGA
FT T -> GQALEAPTQGA (in isoform B).
FT /FTid=VSP_002637.
FT L -> T.
FT /FTid=VAR_003953.
FT N -> V.
FT /FTid=VAR_003954.
FT S -> T (IN REF. 1; CAA32536).
FT
FT CONFLICT 25 25
FT SEQUENCE 374 AA; 42605 MW; 2C2AA8103ECF16E6 CRC64;
FT
FT Query Match 39.5%; Score 374.5; DB 1; Length 374;
FT Best Local Similarity 41.6%; Pred. No. 5.4e-26;
FT Matches 69; Conservative 36; Mismatches 60; Indels 1; Gaps 1;
FT
QY 4 KPKVSLNPPWNRIFKGNVTLTCGNFFVSVSTKWFHNGSLSEETNSLINVNAKPEDS 63
DB 21 KAVITLQPPWVSIFQKENVTLWCCEGPHLPDGSSTQWFNGTAVQISTPSYSIPEASFDS 90
QY 64 GEYKCHQOVNESEPVYLEVFSMDLLLOASAEVWVEGQPLFCHGWNDVYKVIYKDD 123
DB 81 GEYRCQGLSGRSDPIQLHRCWGLLQVSSRVFTEGEPLALRCHAWKQKLVNVDLYRN 140
QY 124 GEALKYWNHNTSITNATVEDSGTYCTGKVMQLDYSEPLNITY 169
DB 141 GKAFKPFHNSNLTKLTNHSNGTYHCSG-MGKHRYTSAGISVTY 185
FT
FT Query Match 39.0%; Score 369; DB 1; Length 404;
FT Best Local Similarity 43.4%; Pred. No. 1.8e-25;
FT Matches 72; Conservative 35; Mismatches 57; Indels 2; Gaps 2;
FT
ID_FCG1_MOUSE STANDARD; PRT; 404 AA.
AC P26151;
DT 01-MAY-1992 (Rel. 22, Created)
DT 01-MAY-1992 (Rel. 22, Last sequence update)
DT 10-OCT-2003 (Rel. 42, Last annotation update)
DE High affinity immunoglobulin gamma Fc receptor I precursor (Fc-gamma RI) (FcRI) (IgG Fc receptor I).
GN FCGRI OR FCG1.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RN SEQUENCE FROM N.A.
RX MEDLINE=90111035; PubMed=2136886;
RA Sears D.W., Osman N., Tate B., McKenzie I.F.C., Hogarth P.M.;
RT "Molecular cloning and expression of the mouse high affinity Fc receptor for IgG."
RL J. Immunol. 144:371-378 (1990).
RL [2]
RX SEQUENCE FROM N.A.
RX MEDLINE=92166399; PubMed=1531670;
RA Osman N., Kozak C.A., McKenzie I.F., Hogarth P.M.;
RT "Structure and mapping of the gene encoding mouse high affinity Fc

```

```

RT gamma RI and chromosomal location of the human Fc gamma RI gene." ;
RL J. Immunol. 148:1570-1575 (1992).
CC !- FUNCTION: Binds to the Fc region of immunoglobulins gamma. High affinity receptor.
CC !- SUBCELLULAR LOCATION: Type I membrane protein.
CC !- TISSUE SPECIFICITY: Macrophage specific.
CC !- SIMILARITY: Contains 3 immunoglobulin-like C2-type domains.
CC !- CAUTION: It is uncertain whether Met-1 or Met-10 is the initiator.
CC
CC This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation - the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/ or send an email to license@isb-sib.ch).
CC
CC EMBL; M31314; AAA40056.1; -.
CC PIR; A46480; A46480.
CC HSSP; P12319; 1ALS.
CC XGD; MGI:95498; Fcgr1.
CC InterPro; IPR007110; Ig-like.
CC InterPro; IPR003598; Ig_C2.
CC Pfam; PF00047; Ig_3.
CC SMART; SM00408; IGC2; 1.
CC PROSITE; PS0835; IG_LIKE; 2.
KW Ig-binding protein; Receptor; Transmembrane; Glycoprotein; Signal;
KW Immunoglobulin domain; Repeat.
KW SIGNAL 1 24
KW CHAIN 25 404
FT HIGH AFFINITY IMMUNOGLOBULIN GAMMA FC
FT RECEPTOR I.
FT EXTRACELLULAR (POTENTIAL).
FT POTENTIAL.
FT CYTOPLASMIC (POTENTIAL).
FT IG-LIKE C2-TYPE 1.
FT IG-LIKE C2-TYPE 2.
FT IG-LIKE C2-TYPE 3.
FT BY SIMILARITY.
FT BY SIMILARITY.
FT N-LINKED (GLCNAC. .) (POTENTIAL).
FT N-LINKED (GLCNAC. .) (POTENTIAL).
FT N-LINKED (GLCNAC. .) (POTENTIAL).
FT N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 28 28
FT CARBOHYD 48 48
FT CARBOHYD 69 69
FT CARBOHYD 168 168
FT CARBOHYD 249 249
FT SEQUENCE 404 AA; 44887 MW; 1C4F0033842767E7 CRC64;
FT
FT Query Match 39.0%; Score 369; DB 1; Length 404;
FT Best Local Similarity 43.4%; Pred. No. 1.8e-25;
FT Matches 72; Conservative 35; Mismatches 57; Indels 2; Gaps 2;
FT
QY 4 KPKVSLNPPWNRIFKGNVTLTCGNFFVSVSTKWFHNGSLSEETNSLINVNAKPEDS 63
DB 31 KAVITLQPPWVSIFQKENVTLWCCEGPHLPDGSSTQWFNGTAVQISTPSYSIPEASFDS 90
QY 64 GEYKCHQOVNESEPVYLEVFSMDLLLOASAEVWVEGQPLFCHGWNDVYKVIYKDD 123
DB 91 GEYRCQGLSGRSDPIQLHRCWGLLQVSSRVFTEGEPLALRCHAWKQKLVNVDLYRN 150
QY 124 GEALKYWNHNTSITNATVEDSGTYCTGKVMQLDYSEPLNITY 169
DB 151 GKSPQF-SSDSEVALKTNLSHSGIYHCSG-TGRHRYTSAGVSIIV 194
FT
FT RESULT 7
FCG3_BOVIN
ID_FCG3_BOVIN STANDARD; PRT; 250 AA.
AC P79107;
DT 30-MAY-2000 (Rel. 39, Created)
DT 30-MAY-2000 (Rel. 39, Last sequence update)
DT 10-OCT-2003 (Rel. 42, Last annotation update)
DE Low affinity immunoglobulin gamma Fc region receptor III precursor (IgG Fc receptor III) (Fc-gamma RI) (FcRIII).
DE

```

GN FCGR3 OR FCGR11.
 OS Bos taurus (Bovine).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
 OC Bovidae; Bovinae; Bos.
 OX NCBI_TaxID=9913;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Lymph node;
 RX MEDLINE=97246739; PubMed=9089104;
 RA Collins R.A., Gelder K.I., Howard C.J.;
 RT "Nucleotide sequence of cattle FCGR11: its identification in
 RT gammadelta T cells."
 RL Immunogenetics 45:440-443(1997).
 CC -!- FUNCTION: IS A RECEPTOR FOR THE FC REGION OF IGG. BINDS COMPLEXED
 CC OR AGGREGATED IGG AND ALSO MONOMERIC IGG. ALSO MEDIATES ANTIBODY-
 CC DEPENDENT CELLULAR TOXICITY (BY SIMILARITY).
 CC -!- SUBCELLULAR LOCATION: Type I membrane protein (Potential).
 CC -!- TISSUE SPECIFICITY: EXPRESSED IN GAMMA-DELTA T CELLS.
 CC -!- SIMILARITY: Contains 2 immunoglobulin-like C2-type domains.
 CC -!- CAUTION: IT IS NOT SURE IF THE VARIANTS ARE DUE TO DIFFERENT
 CC ALLELES OR TO THE EXISTENCE OF AT LEAST TWO GENES.
 CC -----
 CC This SWISS-PROT entry is copyright. It is produced through a collaboration
 CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
 CC the European Bioinformatics Institute. There are no restrictions on its
 CC use by non-profit institutions as long as its content is in no way
 CC modified and this statement is not removed. Usage by and for commercial
 CC entities requires a license agreement (See <http://www.isb-sib.ch/announce/>
 CC or send an email to license@isb-sib.ch)
 CC -----
 DR EMBL; X9595; CA68026.1; -.
 DR HSP; F12319; IALS.
 DR InterPro; IPR007110; IG-like.
 DR PROSITE; PS50835; IG LIKE; 2.
 DR IGG-binding protein; Receptor; Transmembrane; Glycoprotein; Signal;
 KW Immunoglobulin domain; Repeat; Polymorphism.
 FT SIGNAL 1 16
 FT CHAIN 17 250
 FT LOW AFFINITY IMMUNOGLOBULIN GAMMA FC
 FT EXTRACELLULAR (POTENTIAL).
 FT DOMAIN 17 208
 FT TRANSMEM 209 225
 FT DOMAIN 226 250
 FT CYTOPLASMIC (POTENTIAL).
 FT IG-LIKE C2-TYPE 1.
 FT IG-LIKE C2-TYPE 2.
 FT BY SIMILARITY.
 FT DISULFID 47 89
 FT CARBOHYD 56 56
 FT N-LINKED (GLCNAC. .) (POTENTIAL).
 FT CARBOHYD 63 63
 FT N-LINKED (GLCNAC. .) (POTENTIAL).
 FT CARBOHYD 180 180
 FT N-LINKED (GLCNAC. .) (POTENTIAL).
 FT VARIANT 11 11
 FT P -> L.
 FT VARIANT 12 12
 FT K -> R.
 FT VARIANT 107 107
 FT G -> D.
 FT VARIANT 114 114
 FT A -> V.
 FT VARIANT 229 229
 FT V -> I.
 SQ SEQUENCE 250 AA; 28050 MW; D5625139E889E207 CRC64;

Query Match 38.5%; Score 365; DB 1; Length 250;
 Best Local Similarity 42.9%; Pred. No. 2.3e-25;
 Matches 72; Conservative 26; Mismatches 70; Indels 0; Gaps 0;
 QY 2 POKPKVSLNPNWRIKFGENVTLTCNGNFFVSVSTKWFHNGSLSEETNSLSINVAKE 61
 DB 23 PSKAVLLDQWHLVINDRVLTKCQGDYDPVDSIKWANGTLISQTPSPFIADVKVQ 82
 QY 62 DSGYKCOHQOVNSEPVLYLEFSDWLLQASAEVMEGQPLRCHGRNWDVYKVIY 121
 DB 83 DSGEYKCOQGLSPDPSDKLEKLVHGVMLLQVAORVNVGKPIRLKCHSWKTKTVAQVQ 142
 QY 122 KDGEALKYVYENHNISITNATVEDSGTYCTGKWQOLDYSEPLNTV 169

Db 143 RNRGKGYSHGNSDFHPEAKLEHSGYFCRGIQSKNESSSVQITV 190
 RESULT 8
 PCG2_CAVPO STANDARD; PRT; 341 AA.
 ID FCG2_CAVPO Q60513; Q60511; Q60512;
 AC Q60513; Q60498; Q60511; Q60512;
 DT 01-NOV-1997 (Rel. 35, Created)
 DT 01-NOV-1997 (Rel. 35, Last sequence update)
 DT 10-OCT-2003 (Rel. 42, Last annotation update)
 DE Low affinity immunoglobulin gamma Fc region receptor II precursor (Fc-
 DE gamma RII) (FCRII) (IgG Fc receptor II) (fc-gamma-1/gamma-2 receptor).
 GN FCGR2.
 OS Cavia porcellus (Guinea pig).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Hystriognathi; Caviidae; Cavia.
 OX NCBI_TaxID=10141;
 RN [1]
 RP SEQUENCE FROM N.A. (ISOFORM 2R-B1).
 RX MEDLINE=90241239; PubMed=1692213;
 RA Tomimaga M., Sakata A., Ohmura T., Yamashita T., Koyama J., Onoue K.;
 RT "The structure and expression of the guinea pig Fc receptor for IgG1
 RT and IgG2 (Fc gamma 1/gamma 2R)."
 RL Biochem. Biophys. Res. Commun. 168:683-689(1990).
 RN [2]
 RP SEQUENCE FROM N.A. (ISOFORMS 2R-B1; 2R-B2 AND 2R-B3).
 RC STRAIN=JY-1;
 RX MEDLINE=93346746; PubMed=8345193;
 RA Yamashita T., Shinozaki K., Yamashita Y.;
 RT "Expression Cloning of complementary DNA encoding three distinct
 RT isoforms of guinea pig Fc receptor for IgG1 and IgG2."
 RL J. Immunol. 151:2014-2023(1993).
 CC -!- FUNCTION: Binds to the Fc region of immunoglobulins gamma. Low
 CC affinity receptor.
 CC -!- SUBCELLULAR LOCATION: Type I membrane protein.
 CC -!- ALTERNATIVE PRODUCTS:
 CC Name=2R-B3; Isoform=3;
 CC Isoform=Q60513-1; Sequence=Displayed;
 CC Name=2R-B1;
 CC Isoform=Q60513-2; Sequence=VSP_002639;
 CC Name=2R-B2;
 CC Isoform=Q60513-3; Sequence=VSP_002638;
 CC TISSUE SPECIFICITY: Macrophages and polymorphonuclear leukocytes
 CC express preferentially isoform 2R-B1. B lymphocytes express
 CC isoform 2R-B1, isoform 2R-B2 and isoform 2R-B3.
 CC -!- DOMAIN: Contains 1 copy of a cytoplasmic motif that is referred
 CC to as the immunoreceptor tyrosine-based inhibitor motif (ITIM).
 CC This motif is involved in downmodulation of cellular responses.
 CC -!- SIMILARITY: Contains 2 immunoglobulin-like C2-type domains.
 CC -----
 CC This SWISS-PROT entry is copyright. It is produced through a collaboration
 CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
 CC the European Bioinformatics Institute. There are no restrictions on its
 CC use by non-profit institutions as long as its content is in no way
 CC modified and this statement is not removed. Usage by and for commercial
 CC entities requires a license agreement (See <http://www.isb-sib.ch/announce/>
 CC or send an email to license@isb-sib.ch)
 CC -----
 DR EMBL; D13693; BAA02852.1; -.
 DR EMBL; D13692; BAA02851.1; -.
 DR EMBL; D13691; BAA02850.1; -.
 DR EMBL; M35272; AAA37036.1; ALT_INIT.
 DR HSP; F12319; IALS.
 DR InterPro; IPR007110; IG-like.
 DR Pfam; PF00047; Ig; 2.
 DR PROSITE; PS50835; IG LIKE; 2.
 KW IGG-binding protein; Receptor; Transmembrane; Glycoprotein; Signal;
 KW Immunoglobulin domain; Repeat; Alternative splicing.
 FT SIGNAL 1 42
 FT CHAIN 43 341
 FT LOW AFFINITY IMMUNOGLOBULIN GAMMA FC
 FT REGION RECEPTOR II.
 FT EXTRACELLULAR (POTENTIAL).
 FT DOMAIN 43 224

FT TRANSMEM 225 245 POTENTIAL
FT DOMAIN 246 341 CYTOPLASMIC (POTENTIAL)
FT DOMAIN 48 125 IG-LIKE C2-TYPE 1.
FT DOMAIN 131 213 IG-LIKE C2-TYPE 2.
FT SITE 318 323 ITIM MOTIF.
FT DISULFID 71 113 BY SIMILARITY.
FT DISULFID 152 196 BY SIMILARITY.
FT CARBOHYD 73 79 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 106 106 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 180 180 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 187 187 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 195 195 N-LINKED (GLCNAC. .) (POTENTIAL).
FT VARSPLIC 273 301 GEYSVFGGMMSCPLPDGLPEARTDLS -> A (in isoform 2R-B2).
FT FT /FTIG-VSP 002638.
FT FT GNPEHREMGETIPEDGEYSVFGGMMSCPLPDGLPEAR
FT FT TDLS -> A (in isoform 2R-B1).
FT FT /FTIG-VSP 002639.
FT FT Q -> QVLPSTYRFTAKGNDSEYRQ (IN REF. 1).
FT FT CONFLICT 114 114
FT FT SSEQUENCE 341 AA; 37091 MW; 5137E3271D43B84 CRC64;
SQ
Query Match 38.3%; Score 363; DB 1; Length 341;
Best Local Similarity 43.3%; Pred. No. 5e-25;
Matches 73; Conservative 21; Mismatches 74; Indels 0; Gaps 0;
QY 2 POKPKVSLNPPNRIKFGENVILTCNGNPFVSVSTKFWHNGSLSEETNSLNINVAKPE 61
Db 47 PPKAVVLEPPVQLVGRDVTITCEGAPSGNHSTOWLHNGSLIPTQVLPSTYRFTAKGN 106
QY 62 DSEYKCOHQVNEPVLVEFSDMLLQASVVMGQPLFLRCHGNWVDVYVY 121
Db 107 DSEYKCOAGTSLSDPVLVDVSDWLVLQTSOLFQEGDVIIVLRCHSNWNPPLAKVTFY 166
QY 122 KDGELKYYENENISITNATVEDSGTYCTGKWLDYSEPLNITV 169
Db 167 HNGVAKYFISIKNFISIQANSHSGAYNCTGLIGTSHTSPPTIV 214
RESULT 9
FC3A HUMAN
ID FC3A HUMAN STANDARD; PRT; 254 AA.
AC P08637; 1988 (Rel. 08, Created)
DT 01-AUG-1990 (Rel. 15, Last sequence update)
DT 10-OCT-2003 (Rel. 42, Last annotation update)
DE Low affinity immunoglobulin gamma Fc region receptor III-A precursor
DE (IgG Fc receptor III-2) (Fc-gamma RII-alpha) (Fc-gamma RIIIA)
DE (FCRIIA) (Fc-gamma RII) (FCRII) (CD16-A) (FCR-10).
DE FCR3A OR FCG3 OR FCR3 OR IGR3 OR CD16A.
GN Homo sapiens (Human).
OS Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=89328325; PubMed=2526846;
RA Ravetch J.V., Perussia B.;
RT "Alternative membrane forms of Fc gamma RII (CD16) on human natural
RT killer cells and neutrophils. Cell type-specific expression of two
RT genes that differ in single nucleotide substitutions.";
RL J. Exp. Med. 170:481-497 (1989).
RN [2]
RP SEQUENCE OF 1-39 FROM N.A.
RX MEDLINE=95138131; PubMed=7836402;
RA Gessner J.E., Grussemeyer T., Kolanus W., Schmidt R.E.;
RT "The human low affinity immunoglobulin G Fc receptor III-A and III-B
RT genes. Molecular characterization of the promoter regions.";
RL J. Biol. Chem. 270:1350-1356 (1995).
RN [3]
RP VARIANTS ARG-66 AND HIS-66.
RX MEDLINE=96183251; PubMed=8609432;
RA de Haas M., Koene H.R., Kleijer M., de Vries E., Simsek S.,

van Tol M.J.D., Roos D., von dem Borne A.E.G.K.;
RT "A triallelic Fc gamma receptor type IIIA polymorphism influences the
RT binding of human IgG by NK cell Fc gamma RIIIA.";
RL J. Immunol. 156:3948-3955 (1996).
RN [4]
RP VARIANT VAL-157.
RX MEDLINE=97385047; PubMed=9242542;
RA Koene H.R., Kleijer M., Algra J., Roos D., von dem Borne A.E.G.K.,
RA de Haas M.;
RT "Fc gamma RIIIA-158V/F polymorphism influences the binding of IgG by
RT natural killer cell Fc gamma RIIIA, independently of the Fc
RT gamma RIIIA-48L/R/H phenotype.";
RL Blood 90:1109-1114 (1997).
RN [5]
RP VARIANT VAL-176.
RX MEDLINE=97426467; PubMed=9276722;
RA Wu J., Ederberg J.C., Redecha P.B., Bansal V., Guyre P.M., Coleman K.,
RA Salmon J.E., Kimberly R.P.;
RT "A novel polymorphism of Fc gamma RIIIA (CD16) alters receptor function
RT and predisposes to autoimmune disease.";
RL J. Clin. Invest. 100:1059-1070 (1997).
CC -!- FUNCTION: RECEPTOR FOR THE FC REGION OF IGG. BINDS COMPLEXED OR
CC AGGREGATED IGG AND ALSO MONOMERIC IGG. MEDIATES ANTIBODY-DEPENDENT
CC CELLULAR CYTOTOXICITY (ADCC) AND OTHER ANTIBODY-DEPENDENT
CC RESPONSES, SUCH AS PHAGOCYTOSIS.
CC -!- SUBUNIT: EXISTS AS A HETERO-OLIGOMERIC RECEPTOR COMPLEX WITH FC
CC EPSILON RECEPTOR I GAMMA SUBUNIT AND / OR THE CD3 ZETA SUBUNIT.
CC -!- SUBCELLULAR LOCATION: Type I membrane protein (Potential). Exists
CC also as a soluble receptor.
CC -!- TISSUE SPECIFICITY: Expressed on natural killer cells,
CC macrophages, subpopulation of T cells, immature thymocytes and
CC placental trophoblasts.
CC -!- PTM: Glycosylated. Contains high mannose- and complex-type
CC oligosaccharides.
CC -!- PTM: The soluble form is produced by a proteolytic cleavage.
CC -!- POLYMORPHISM: Isoform Val-157 shows a higher binding capacity of
CC IGG1, IGG3 and IGG4 compared with isoform Phe-157. Alleles Leu-66
CC and Phe-157, and alleles His-66 / Arg-66 and Val-157 are in
CC linkage disequilibrium.
CC -!- MISCELLANEOUS: ENCODED BY ONE OF TWO NEARLY IDENTICAL GENES:
CC FCR3A (SHOWN HERE) AND FCR3B WHICH ARE EXPRESSED IN A TISSUE-
CC SPECIFIC MANNER. THE PHE-203 IN III-A DETERMINES THE TRANSMEMBRANE
CC DOMAINS WHEREAS THE SER-203 IN III-B DETERMINES THE GPI-ANCHORING.
CC -!- SIMILARITY: Contains 2 immunoglobulin-like C2-type domains.
CC -!- DATABASE: NAME=PROW; NCBI=cd guide CD16A entry;
CC WWW="http://www.ncbi.nlm.nih.gov/prow/cd/cd16a.htm".
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use by non-profit institutions as long as its content is in no way
CC modified and this statement is not removed. Usage by and for commercial
CC entities requires a license agreement (see http://www.isb-sib.ch/announce/
CC or send an email to license@isb-sib.ch).
CC
CC EMBL; X52645; CAA36870.1; -;
CC EMBL; Z46222; CAA86295.1; -;
CC PIR; JLO107; JLO107.
CC HSP; P12319; IALS.
CC Genew; HGNC:3619; FCR3A.
CC MIM; 146740; -;
CC GO; GO:0005886; C:plasma membrane; TAS.
CC GO; GO:0006955; P:immune response; TAS.
CC InterPro; IPR007110; IG-like.
CC InterPro; IPR003599; IG.
CC Pfam; PF00447; ig; 2.
CC SMART; SM00409; IG; 2.
CC PROSITE; PS00835; IG_LIKE; 2.
CC IgG-binding protein; Receptor; Transmembrane; Glycoprotein; Signal;
KW Immunoglobulin domain; Repeat; Multigene family; Polymorphism.
RN SIGNAL 1 16
RN CHAIN 17 254
RN REGION RECEPTOR III-A.

FT DOMAIN 17 208 EXTRACELLULAR (POTENTIAL).
 FT TRANSMEM 209 224 POTENTIAL.
 FT DOMAIN 230 234 CYTOPLASMIC (POTENTIAL).
 FT DOMAIN 24 105 IG-LIKE C2-TYPE 1.
 FT DOMAIN 107 189 IG-LIKE C2-TYPE 2.
 FT DISULFID 47 89 BY SIMILARITY.
 FT DISULFID 128 172 BY SIMILARITY.
 FT CARBOHYD 56 56 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 63 63 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 92 92 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 180 180 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 187 187 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT VARIANT 66 66 L -> R.
 FT VARIANT 66 66 /FTID=VAR_008799.
 FT VARIANT 66 66 L -> H.
 FT VARIANT 157 157 /FTID=VAR_008800.
 FT VARIANT 176 176 F -> V.
 FT VARIANT 176 176 F -> V (in dbSNP:396991).
 FT SEQUENCE 254 AA; 29089 MW; D38D178D32C67337 CRC64;
 Query Match 38.1%; Score 361; DB 1; Length 254;
 Best Local Similarity 44.0%; Pred. No. 5.3e-25;
 Matches 73; Conservative 26; Mismatches 67; Indels 0; Gaps 0;
 QY 4 KPKVSLNPPNRIKGVNTLTGNNFFVSTKWFHNGSLSEETNSLNINAKFEDS 63
 DB 25 KAVFLEPQWTVLEKDSVTLKCGAYSPDNSTQWFHNSLISSQASSFIDATVDD 84
 QY 64 GEYKQHQVNESEPVYLEVFSDDLLOQASAEVVMGQPLFLRCHGRWMDVYKVIYK 123
 DB 85 GEYRCQTNLTSLSDPVQLEVHIGWLLQAPRWFKEDPIHLRCHSWKNTALHKVTVLQ 144
 QY 124 GEALKYVYENHISITNATVEDSTVYCTGKVMQLDYSEPLNITV 169
 DB 145 GGRKRFHNSDFYIPKATLKDGSYFCRGLFGSKVNSSETVNITI 190
 RESULT 10
 FCQ3_PIG STANDARD; PRT; 257 AA.
 AC Q28942; Q28940; Q28941;
 DT 01-NOV-1997 (Rel. 35, Created)
 DT 01-NOV-1997 (Rel. 35, Last sequence update)
 DT 10-OCT-2003 (Rel. 42, Last annotation update)
 DE Low affinity immunoglobulin gamma Fc region receptor III precursor
 DE (IgG Fc receptor III) (Fc-gamma RIII) (FCRIII) (Cytolytic trigger
 DE molecule G7).
 GN FCGR3.
 OS Sus scrofa (Pig).
 OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus.
 OC NCBI_TaxID=9823;
 RN [1]
 RP SEQUENCE FROM N.A., AND SEQUENCE OF 27-47; 92-107 AND 179-188.
 RC STRAIN=Minnesota miniature swine;
 RX MEDLINE=94358430; PubMed=8077673;
 RA Halloran P.J., Sweeney S.E., Strohmeyer C.M., Kim Y.B.;
 RT "Molecular cloning and identification of the porcine cytolytic
 RT trigger molecule G7 as a Fc gamma RIII alpha (CD16) homologue";
 RL J. Immunol. 153:2631-2641(1994).
 CC -1- FUNCTION: Receptor for the Fc region of complexed immunoglobulins
 CC gamma. Low affinity receptor.
 CC -1- SUBUNIT: FORMS A COMPLEX WITH NK-E.
 CC -1- SUBCELLULAR LOCATION: Type I membrane protein (Potential).
 CC -1- TISSUE SPECIFICITY: FOUND IN POLYMORPHONUCLEAR CELLS (PMN), PBMC,
 CC MACROPHAGES, SPLEEN, AND AT LOW LEVELS IN LYMPH NODES BUT NOT IN
 CC THYMUS OR LIVER.
 CC -1- SIMILARITY: Contains 2 immunoglobulin-like C2-type domains.
 CC
 CC This SWISS-PROT entry is copyright. It is produced through a collaboration
 CC between the Swiss Institute of Bioinformatics and the EMBL outstation -

the European Bioinformatics Institute. There are no restrictions on its
 use by non-profit institutions as long as its content is in no way
 modified and this statement is not removed. Usage by and for commercial
 entities requires a license agreement (See <http://www.isb-sib.ch/announce/>
 or send an email to license@isb-sib.ch).

 CC EMBL; U08993; AAA57190.1; -;
 CC EMBL; U08991; AAA57188.1; -;
 CC EMBL; U08992; AAA57189.1; -;
 CC HSP; P12319; IALS.
 CC InterPro; IPR007110; Ig-like.
 CC InterPro; IPR003599; Ig.
 CC Pfam; PF00047; ig_2
 CC SMART; SM00409; ig_2;
 CC PROSITE; PS0835; IG_LIKE; 2.
 CC IgG-binding protein; Receptor; Transmembrane; Glycoprotein; Signal;
 KW Immunoglobulin domain; Repeat.
 FT SIGNAL 1 19 POTENTIAL.
 FT CHAIN 20 257 LOW AFFINITY IMMUNOGLOBULIN GAMMA FC
 FT DOMAIN 20 209 REGION RECEPTOR III.
 FT TRANSMEM 210 230 EXTRACELLULAR (POTENTIAL).
 FT DOMAIN 231 257 POTENTIAL.
 FT DOMAIN 25 104 CYTOPLASMIC (POTENTIAL).
 FT DOMAIN 108 190 IG-LIKE C2-TYPE 1.
 FT DISULFID 48 90 IG-LIKE C2-TYPE 2.
 FT DISULFID 129 173 BY SIMILARITY.
 FT CARBOHYD 64 64 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 134 134 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 162 162 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 181 181 N-LINKED (GLCNAC. . .) (IN CLONE 334.8)
 FT VARIANT 55 55 R -> G (IN CLONE 284.4).
 FT VARIANT 149 149 K -> M (IN CLONE 334.8).
 FT VARIANT 181 181 D -> N (IN CLONE 334.8).
 FT VARIANT 186 186 P -> A (IN CLONE 334.8).
 FT SEQUENCE 257 AA; 29062 MW; 1D038CC1552B97CB CRC64;
 Query Match 38.0%; Score 360; DB 1; Length 257;
 Best Local Similarity 41.7%; Pred. No. 6.6e-25;
 Matches 70; Conservative 33; Mismatches 65; Indels 0; Gaps 0;
 QY 2 POKPKVSLNPPNRIKGVNTLTGNNFFVSTKWFHNGSLSEETNSLNINAKFE 61
 DB 24 PPKSVVILDPWDRLLXDSVTLKCGAYPRDDSDSTWRWNGTLISNKASSYSITATVG 83
 QY 62 DSGEYKQHQVNESEPVYLEVFSDDLLOQASAEVVMGQPLFLRCHGRWMDVYKVIY 121
 DB 84 NSGETCTKGLSAQSDPLRLVYKGNLQLQAPRWVQGESIRLIRCHTWKNTITQKQYVF 143
 QY 122 KDGEALKYVYENHISITNATVEDSTVYCTGKVMQLDYSEPLNITV 169
 DB 144 QNGMGKFSHQNFVHPIPNATLKDGSYFCRGLFGSKVNSSETVNITI 191
 RESULT 11
 FCQ2_RAT STANDARD; PRT; 285 AA.
 ID FCQ2_RAT
 AC Q63203;
 DT 01-NOV-1997 (Rel. 35, Created)
 DT 01-NOV-1997 (Rel. 35, Last sequence update)
 DT 15-MAR-2004 (Rel. 43, Last annotation update)
 DE Low affinity immunoglobulin gamma Fc region receptor II precursor (Fc-
 DE gamma RII) (FCRII) (IG Fc receptor II beta).
 GN FCGR2.
 OS Rattus norvegicus (Rat).
 OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
 OC NCBI_TaxID=10116;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=94009652; PubMed=8405417;
 RA Bocek P., Pecht I.;

```

RT "Cloning and sequence of the cDNA coding for rat type II Fc gamma
RT receptor of mast cells."
RL FEBS Lett. 331:86-90(1993).
CC -!- FUNCTION: Binds to the Fc region of immunoglobulins gamma. Low
CC affinity receptor. By binding to IgG it initiates cellular
CC responses against pathogens and soluble antigens.
CC -!- SUBCELLULAR LOCATION: Type I membrane protein.
CC -!- DOMAIN: Contains 1 copy of a cytoplasmic motif that is referred
CC to as the immunoreceptor tyrosine-based inhibitor motif (ITIM).
CC This motif is involved in downmodulation of cellular responses.
CC The phosphorylated ITIM motif binds to the SH2 domain of
CC PTPN6/SHP-1.
CC -!- SIMILARITY: Contains 2 immunoglobulin-like C2-type domains.
CC
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation
CC the European Bioinformatics Institute. There are no restrictions on its
CC use by non-profit institutions as long as its content is in no way
CC modified and this statement is not removed. Usage by and for commercial
CC entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC or send an email to license@isb-sib.ch).
CC
CC EMBL; X73371; CAA51788.1; -.
CC PIR; S36903; S36903.
CC HSSP; P12319; IALS.
CC InterPro; IPR007110; Ig-like.
CC InterPro; IPR003599; Ig.
CC Pfam; PF00047; Ig; 2.
CC SMART; SM00409; IG; 2.
CC PROSITE; PS00835; IG_LIKE; 2.
CC Ig-binding protein; Receptor; Transmembrane; Glycoprotein; Signal;
CC Immunoglobulin domain; Repeat.
CC SIGNAL 1 31
CC CHAIN 32 285
CC
CC LOW AFFINITY IMMUNOGLOBULIN GAMMA Fc
CC REGION RECEPTOR II
CC EXTRACELLULAR (POTENTIAL).
CC TRANSMEM
CC 213 233
CC POTENTIAL.
CC CYTOPLASMIC (POTENTIAL).
CC DOMAIN 234 285
CC 36 118
CC IG-LIKE C2-TYPE 1.
CC DOMAIN 119 201
CC 201 267
CC IG-LIKE C2-TYPE 2.
CC SITE 262 267
CC ITIM MOTIF.
CC DISULFID 59 101
CC BY SIMILARITY.
CC DISULFID 140 184
CC CARBOHYD 67 67
CC N-LINKED (GLCNAC. . .) (POTENTIAL).
CC CARBOHYD 75 75
CC N-LINKED (GLCNAC. . .) (POTENTIAL).
CC CARBOHYD 86 86
CC N-LINKED (GLCNAC. . .) (POTENTIAL).
CC CARBOHYD 94 94
CC N-LINKED (GLCNAC. . .) (POTENTIAL).
CC CARBOHYD 168 168
CC N-LINKED (GLCNAC. . .) (POTENTIAL).
CC CARBOHYD 175 175
CC N-LINKED (GLCNAC. . .) (POTENTIAL).
CC SSSEQUENCE 285 AA; 32047 MW; 255540A584CFFA0A CRC64;
CC
CC Query Match 37.8%; Score 358; DB 1; Length 285;
CC Best Local Similarity 40.4%; Pred. No. 1.1e-24;
CC Matches 67; Conservative 33; Mismatches 66; Indels 0; Gaps 0;
CC
CC QY 4 KPVKSLNPPNRRIFKGNVTLTGNNFFVSTKVFHNGSLSEETNSSLNIVNAKFEPS 63
CC DB 37 KAVVLEPPWIOVLKEDTVTLMCEGTHNTKNCSTQWFHNGSSITWHQAQANYTFKATVND 96
CC
CC QY 64 GEYKCOHQVNESEPPVLEFVSFLLQASAEVVMGQPLFLFCHGRNNDVVKVYKXD 123
CC DB 97 GEYRCRMEETGISEPHLGVISDWLLQTSQLVFEEGEITLCHSKWKQLTKVLLFQN 156
CC
CC QY 124 GEALKYWNHNISITNATVEDSGTYCTGKWQWLDYSEPLNTV 169
CC DB 157 GKPVRYHHQSNFSPKXNHSNGNYKAYLGRTHVSKXPVTIV 202
CC
CC RESULT 12
CC FC3B HUMAN
CC ID FC3B HUMAN STANDARD; PRT; 233 AA.
CC AC O75015;
CC DT 30-MAY-2000 (Rel. 39, Created)

```

```

DT 30-MAY-2000 (Rel. 39, Last sequence update)
DT 15-MAY-2004 (Rel. 43, Last annotation update)
DE Low affinity immunoglobulin gamma Fc region receptor III-B precursor
DE (IgG Fc receptor III-1) (Fc-gamma RIII-beta) (Fc-gamma RIIIB)
DE (FCRIIB) (Fc-gamma RIII) (FCRII) (CD16-B) (FCR-10).
DE FCR3B OR FC3 OR FCR3 OR IGF3 OR CD16B.
DE Homo sapiens (Human).
DE Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
DE Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
DE NCBI_TaxID=9606;
DE [1]
DE SEQUENCE FROM N.A. (VARIANT NA-2).
DE MEDLINE=89328325; PubMed=2526846;
DE Ravetch J.V., Perussia B.;
DE "Alternative membrane forms of Fc gamma RIII(CD16) on human natural
DE killer cells and neutrophils. Cell type-specific expression of two
DE genes that differ in single nucleotide substitutions."
DE J. Exp. Med. 170:481-497(1989).
DE [2]
DE SEQUENCE FROM N.A. (VARIANT NA-2).
DE TISSUE=Placenta;
DE MEDLINE=88232937; PubMed=2967436;
DE Simmons D., Seed B.;
DE "The Fc gamma receptor of natural killer cells is a phospholipid-
DE linked membrane protein."
DE Nature 333:568-570(1988).
DE [3]
DE ERRATUM.
DE Simmons D., Seed B.;
DE Nature 340:662-662(1989).
DE [4]
DE SEQUENCE FROM N.A. (VARIANT NA-1).
DE TISSUE=Leukocyte;
DE MEDLINE=89128838; PubMed=2521732;
DE Peltz G.A., Grundy H.O., Lebo R.V., Yssel H., Barsh G.S., Moore K.W.;
DE "Human Fc-gamma-RIII: Cloning, expression, and identification of the
DE chromosomal locus of two Fc receptors for IgG."
DE Proc. Natl. Acad. Sci. U.S.A. 86:1013-1017(1989).
DE [5]
DE SEQUENCE OF 1-72 FROM N.A. (VARIANT NA-2).
DE TISSUE=Placenta;
DE MEDLINE=95138131; PubMed=7836402;
DE Gesener J.E., Grussemeyer T., Kolanus W., Schmidt R.E.;
DE "The human low affinity immunoglobulin G Fc receptor III-A and III-B
DE genes. Molecular characterization of the promoter regions."
DE J. Biol. Chem. 270:1350-1361(1995).
DE [6]
DE X-RAY CRYSTALLOGRAPHY (3.2 ANGSTROMS) IN COMPLEX WITH IGG1 Fc.
DE MEDLINE=20372189; PubMed=10917521;
DE Sonderrmann P., Huber R., Oosthuizen V., Jacob U.;
DE "The 3.2-A crystal structure of the human IgG1 Fc fragment-Fc
DE gammaRIII complex."
DE Nature 406:267-273(2000).
DE [7]
DE X-RAY CRYSTALLOGRAPHY (1.8 ANGSTROMS) OF 19-192.
DE MEDLINE=20471519; PubMed=11021536;
DE Zhang Y., Boesen C.C., Radaev S., Brooks A.G., Fridman W.H.,
DE Sautes-Fridman C., Sun P.D.;
DE "Crystal structure of the extracellular domain of a human Fc gamma
DE RIII."
DE Immunity 13:387-395(2000).
DE [8]
DE VARIANT SH ASP-78
DE MEDLINE=97180159; PubMed=9028335;
DE Bux J., Stein E.L., Bierling F., Fromont P., Clay M., Stroncek D.,
DE Santoso S.;
DE "Characterization of a new alloantigen (SH) on the human neutrophil Fc
DE gamma receptor IIIB."
DE Blood 89:1027-1034(1997).
DE -!- FUNCTION: RECEPTOR FOR THE FC REGION OF IMMUNOGLOBULINS GAMMA. LOW
DE AFFINITY RECEPTOR. BINDS COMPLEXED OR AGGREGATED IGG AND ALSO
DE MONOMERIC IGG. CONTRARY TO III-A, IS NOT CAPABLE TO MEDIATE
DE ANTIBODY-DEPENDENT CYTOTOXICITY AND PHAGOCYTOSIS. MAY SERVE AS A

```

```

FT VARIANT 78 78 A -> D (in allele SH).
FT FT /FTID=VAR_008902.
FT VARIANT 82 82 N -> D (in allele NA-1).
FT FT /FTID=VAR_003957.
FT VARIANT 106 106 I -> V (in allele NA-1).
FT FT /FTID=VAR_003964.
FT SQ SEQUENCE 233 AA; 26216 MW; 7AB5159432761726 CRC64;

Query Match 37.7%; Score 357; DS 1; Length 233;
Best Local Similarity 44.0%; Pred. No. 1.le-24;
Matches 73; Conservative 25; Mismatches 68; Indels 0; Gaps 0;

QY 4 KPKVSLNPPNRIKPGENVLTTCGNPNFFVSTKTFHNGSLSEETNSLNIINAKFPDS 63
DB 25 KAVFELEPQWVSLVKRDSVTLKCGAYSPEDNSTQMFHNSLTSQASSYFFDAATVND 84
QY 64 GEYKQCHOQVNESBPVLYEVFSOWLLQQAAYVMGQPLFLRCHGRWNVDYKVIYVKD 123
DB 85 GEYRCQTNLSTLSDPVQLEVHIGWLLQLQAPRWVKEEDPHLRCHSKNKTALHKVYQLN 144

QY 124 GEALKYWYENNISITWATVEDSGTYICTCKVQWLDYSEPLNIV 169
DB 145 GKDRKYPFHNSDFPIKATLKSGSYFCRGLVGSKNVSSETNITI 190

RESULT 13
FC22_MOUSE
ID FC22_MOUSE STANDARD; PRT; 330 AA.
AC P08101; P06102; P12316; P97917; Q06938; Q06940; Q61170;
AC Q61558;
DT 01-AUG-1988 (Rel. 08, Created)
DT 01-NOV-1997 (Rel. 35, Last sequence update)
DT 10-OCT-2003 (Rel. 42, Last annotation update)
DE Low affinity immunoglobulin gamma Fc region receptor II precursor (Fc-
DE gamma RII) (FCRII) (IGF Fc receptor II beta) (Fc gamma receptor IIB)
DE (FC-gamma-RIIB).
DE FCGR2 OR FCGR2B OR LY-17.
GN Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RN SEQUENCE FROM N.A., AND SEQUENCE OF 30-51 (ISOFORM IIB1 AND IIB2).
RX MEDLINE=87042761; PubMed=2946078;
RX Ravetch J.V., Luster A.D., Weinshank R., Kochan J., Pavlovic A.,
RX Portnoy D.A., Hulmes J., Pan Y.-C.E., Unkeless J.C.;
RX "Structural heterogeneity and functional domains of murine
RX immunoglobulin G Fc receptors.";
RX Science 234:718-725 (1996).
RN [2]
RN SEQUENCE FROM N.A. (ISOFORM IIB2).
RP TISSUE=Macrophage;
RC MEDLINE=87065089; PubMed=3024012;
RX Lewis V.A., Koch T., Plutner H., Mellman I.;
RX "A complementary DNA clone for a macrophage-lymphocyte Fc receptor.";
RX Nature 324:372-375 (1986).
RN [3]
RN SEQUENCE FROM N.A., AND PARTIAL SEQUENCE (ISOFORM IIB1).
RP MEDLINE=87306729; PubMed=2957319;
RX Hogarth P.M., Hibbs M.L., Bonadonna L., Scott B.M., Witort E.,
RX Pieterz G.A., McKenzie I.F.C.;
RX "The mouse Fc receptor for IgG (Ly-17): molecular cloning and
RX specificity.";
RX Immunogenetics 26:161-168 (1987).
RN [4]
RN SEQUENCE FROM N.A. (ISOFORM IIB1), AND VARIANTS.
RP STRAIN=BALB/c; TISSUE=Spleen;
RC MEDLINE=90202030; PubMed=2136587;
RX Ian M., Quelch K., Deacon N.J., McKenzie I.F., Hogarth P.M.;
RX "Identification of the mouse beta Fc gamma RII polymorphism by direct
RX sequencing of amplified genomic DNA.";
RX Immunogenetics 31:202-206 (1990).
RN [5]

```


100

This Page Blank (uspio)

Db 21 KAVITLQPPWVSFQEEVTLHCEVHLPGSSSTQWFLNGTATQTSTPSYRITSASVND 80
Qy 64 GEYKCOHQVNESEPVYLEVSDMLLQASAEVWNEGQPLFLRCHGWRNMDVYKVIYKD 123
Db 81 GEYRCQGLSGRSDPIQLEIHRGWLMLLQVSSRVTEGEPLALRCHAWKDKLVNVLVYRN 140
Qy 124 GEALKYWEENHNISITNATVEDSGTYCTGKQVWQLDYSEPLNLT 169
Db 141 GRAKFFHNSNLTILKTNHSHNGTYHCSG-MGKHRYTSAGISVT 185

RESULT 5
Q92637 ID Q92637 PRELIMINARY; PRT; 280 AA.
AC Q92637;
DT 01-FEB-1997 (TRENBLrel. 02, Created)
DT 01-FEB-1997 (TRENBLrel. 02, Last sequence update)
DT 01-OCT-2003 (TRENBLrel. 25, Last annotation update)
DE FC gamma receptor I.
GN B1
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE-Blood;
RX MEDLINE=93055454; PubMed=1430234;
RA Forges A.J., Redecha P.B., Doebele R., Pan L.C., Salmon J.E.,
RA Kimberly R.P.;
RT "Novel Fc gamma receptor I family gene products in human mononuclear
RT cells";
RL J. Clin. Invest. 90:2102-2109(1992).
DR EMBL; L03419; AAA35825.1; -.
DR PIR; I55577; I55577.
DR GO; GO:0005886; C:plasma membrane; NAS.
DR GO; GO:0003793; F:defense/immunity protein activity; NAS.
DR GO; GO:0016489; F:immunoglobulin receptor activity; NAS.
DR GO; GO:0006955; P:immune response; NAS.
DR InterPro; IPR003599; IG.
DR InterPro; IPR007110; IG-like.
DR SMART; SM00409; IG; 2.
DR PROSITE; PS50835; IG_LIKE; 2.
KW Receptor.
SQ SEQUENCE 280 AA; 32232 MW; C6C6C45AE3D345C6 CRC64;

Query Match 39.2%; Score 371; DB 4; Length 280;
Best Local Similarity 43.3%; Pred. No. 7.3e-26;
Matches 65; Conservative 32; Mismatches 53; Indels 0; Gaps 0;
Qy 4 KPKVSLNPPWNRIFKGNVTLTCGNFFSVSTKWFHNGSLSEETNSLNIVNAKPEDS 63
Db 21 KAVITLQPPWVSFQEEVTLHCEVHLPGSSSTQWFLNGTATQTSTPSYRITSASVND 80
Qy 64 GEYKCOHQVNESEPVYLEVSDMLLQASAEVWNEGQPLFLRCHGWRNMDVYKVIYKD 123
Db 81 GEYRCQGLSGRSDPIQLEIHRGWLMLLQVSSRVTEGEPLALRCHAWKDKLVNVLVYRN 140
Qy 124 GEALKYWEENHNISITNATVEDSGTYCTG 153
Db 141 GRAKFFHNSNLTILKTNHSHNGTYHCSG 170

RESULT 6
Q92495 ID Q92495 PRELIMINARY; PRT; 375 AA.
AC Q92495;
DT 01-FEB-1997 (TRENBLrel. 02, Created)
DT 01-FEB-1997 (TRENBLrel. 02, Last sequence update)
DT 01-OCT-2003 (TRENBLrel. 25, Last annotation update)
DE FC gamma receptor type I (Fc gamma RIB=Fc gamma receptor).

GN CD64 OR FC-GAMMA>RIB.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE-Blood;
RA Benesh P.D., Sastry K.N., Iyer R.R., Eichbaum Q.G., Raveh D.,
RA Ezekowitz A.B.;
RL Submitted (DEC-1992) to the EMBL/GenBank/DBSJ databases.
RN [2]

RP SEQUENCE OF 1-224 FROM N.A.
RX MEDLINE=93018827; PubMed=1402657;
RA Benesh P.D., Sastry K., Iyer R.R., Eichbaum Q.G., Raveh D.P.,
RA Ezekowitz R.A.;
RT "Definition of interferon gamma-response elements in a novel human Fc
RT gamma receptor gene (Fc gamma RIB) and characterization of the gene
RT structure";
RL J. Exp. Med. 176:1115-1123(1992).
DR EMBL; M91555; AAA58414.1; -.
DR EMBL; M91550; AAA58414.1; JOINED.
DR EMBL; M91551; AAA58414.1; JOINED.
DR EMBL; M91552; AAA58414.1; JOINED.
DR EMBL; M91553; AAA58414.1; JOINED.
DR EMBL; M91554; AAA58414.1; JOINED.
DR EMBL; M91555; AAA58414.1; JOINED.
DR EMBL; S45709; AAD13842.1; -.
DR EMBL; S45707; AAD13842.1; JOINED.
DR EMBL; S45708; AAD13842.1; JOINED.
DR EMBL; S45704; AAD13842.1; JOINED.
DR EMBL; S45705; AAD13842.1; JOINED.
DR InterPro; IPR007110; IG-like.
DR InterPro; IPR003598; IG_c2.
DR Pfam; PF00047; IG; 3.
DR SMART; SM00408; IGC2; 1.
DR PROSITE; PS50835; IG_LIKE; 3.
KW Immunoglobulin domain.
SQ SEQUENCE 375 AA; 42881 MW; A84D464C70DD0F91 CRC64;

Query Match 39.2%; Score 371; DB 4; Length 375;
Best Local Similarity 43.3%; Pred. No. 1.1e-25;
Matches 65; Conservative 32; Mismatches 53; Indels 0; Gaps 0;
Qy 4 KPKVSLNPPWNRIFKGNVTLTCGNFFSVSTKWFHNGSLSEETNSLNIVNAKPEDS 63
Db 21 KAVITLQPPWVSFQEEVTLHCEVHLPGSSSTQWFLNGTATQTSTPSYRITSASVND 80
Qy 64 GEYKCOHQVNESEPVYLEVSDMLLQASAEVWNEGQPLFLRCHGWRNMDVYKVIYKD 123
Db 81 GEYRCQGLSGRSDPIQLEIHRGWLMLLQVSSRVTEGEPLALRCHAWKDKLVNVLVYRN 140
Qy 124 GEALKYWEENHNISITNATVEDSGTYCTG 153
Db 141 GRAKFFHNSNLTILKTNHSHNGTYHCSG 170

RESULT 7
Q9WZT0 ID Q9WZT0 PRELIMINARY; PRT; 349 AA.
AC Q9WZT0;
DT 01-OCT-2000 (TRENBLrel. 15, Created)
DT 01-OCT-2000 (TRENBLrel. 15, Last sequence update)
DT 01-OCT-2003 (TRENBLrel. 25, Last annotation update)
DE FC gamma receptor I.
OS Bos taurus (Bovine).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovoidea;
OC Bovidae; Bovinae; Bos.
OX NCBI_TaxID=9913;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=20349800; PubMed=10889306;
RA Yan Y., Li X., Wang A., Zhang G.;


```

DR SMART; SM00409; IG; 3.
KW PROSITE; PS0835; IG_LIKE; 4.
FT NON_TER 318 318
SQ SEQUENCE 318 AA; 36270 MW; 1E0881423F2B4A4E CRC64;

Query Match
Best Local Similarity 37.5%; Score 355; DB 11; Length 318;
Matches 67; Conservative 32; Mismatches 67; Indels 0; Gaps 0;

QY 4 KPKVSLPPNRIKFGENVLTCTGNFFVSTKWFHNGSLSEETNSLNIVNAKPEDS 63
DB 151 KAVVLEPFWQLKEDVTLMCEGHTNKKCSQWTFHNGSSIHQAQANTFTKATVND 210

QY 64 GEYKCOHQVNESEPVYLEVFSWLLLOQASAEVVMGQPLFLRCHGWRNWDVYKVIYKD 123
DB 211 GEYRCQNLSTLSPVQLEVHIGWLLLOQAPRWVFEEDPHLRCHSKWNTALHKVYLQN 270

QY 124 GEALKYWNENISITNATVDSGTYYCTGKWQLDYSEPLNITV 169
DB 271 GKPVRYHQSNSFIPKANSHSGNYCKAYGLRGTMHVSKVETITV 316

RESULT 11
Q9UPV7
ID Q9UPY7 PRELIMINARY; PRT; 233 AA.
AC Q9UPY7;
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE FC-gamma receptor IIIB (CD 16).
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=20487377; PubMed=11034564;
RA Watanabe Y., Shinada E., Fujiwara K., Niihara H., Shimano K.,
RA Mitunaga S., Tadokoro K., Jui T.;
RT "Nucleotide sequence of a new Fc gamma receptor IIIB allele that codes
RT for a neutrophil antigen.";
RL Tissue Antigens 56:272-275(2000).
DR EMBL; AB025256; BAA81803.1; -.
DR GO; GO:0004872; F:receptor activity; IEA.
DR InterPro; IPR003599; IG-like.
DR InterPro; IPR007110; IG-like.
DR Pfam; PF00047; IG; 2.
DR SMART; SM00409; IG; 2.
DR PROSITE; PS0835; IG_LIKE; 1.
KW Receptor.
FT VARIANT 54 54 K -> E.
SQ SEQUENCE 233 AA; 26215 MW; 74B51B909272B388 CRC64;

Query Match
Best Local Similarity 37.3%; Score 353; DB 4; Length 233;
Matches 72; Conservative 26; Mismatches 58; Indels 0; Gaps 0;

QY 4 KPKVSLPPNRIKFGENVLTCTGNFFVSTKWFHNGSLSEETNSLNIVNAKPEDS 63
DB 25 KAVVLEPFWQLKEDVTLMCEGHTNKKCSQWTFHNGSSIHQAQANTFTKATVND 84

QY 64 GEYKCOHQVNESEPVYLEVFSWLLLOQASAEVVMGQPLFLRCHGWRNWDVYKVIYKD 123
DB 85 GEYRCQNLSTLSPVQLEVHIGWLLLOQAPRWVFEEDPHLRCHSKWNTALHKVYLQN 144

QY 124 GEALKYWNENISITNATVDSGTYYCTGKWQLDYSEPLNITV 169
DB 145 GKDRKYFHNSDFHPIKATLKDSSGYFCRGLGVSKVNSSTVNITI 190

RESULT 12
Q9R477

```

```

ID Q9R477 PRELIMINARY; PRT; 249 AA.
AC Q9R477;
DT 01-JUN-2002 (TrEMBLrel. 21, Created)
DT 01-JUN-2002 (TrEMBLrel. 21, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Transmembrane receptor CD16-2.
GN FCRL3.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6; TISSUE=Liver;
RA Mechetina L.V., Najakshin A.M., Alabyev B.Y., Chikaev N.A.,
RA Taranin A.V.;
RT "Identification of CD16-2, a novel mouse receptor homologous to
RT CD16/FCGR1II.";
RL Submitted (APR-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF499613; AAM19249.1; -.
DR MGD; MGI:2179523; Fcrl3.
DR GO; GO:0004872; F:receptor activity; IEA.
DR InterPro; IPR003599; IG-like.
DR InterPro; IPR007110; IG-like.
DR Pfam; PF00047; IG; 2.
DR SMART; SM00409; IG; 2.
DR PROSITE; PS0835; IG_LIKE; 2.
KW Receptor.
SQ SEQUENCE 249 AA; 28382 MW; 3DEAF3D935BEP5CD CRC64;

Query Match
Best Local Similarity 37.0%; Score 350; DB 11; Length 249;
Matches 69; Conservative 31; Mismatches 67; Indels 0; Gaps 0;

QY 3 QKPKVSLPPNRIKFGENVLTCTGNFFVSTKWFHNGSLSEETNSLNIVNAKPED 62
DB 23 QKAVNLDPKVTVLEEDSVTLRCQTFSPEDNSIKWFHNSLIHQDANYVIQSRVXD 82

QY 63 SGEYKCOHQVNESEPVYLEVFSWLLLOQASAEVVMGQPLFLRCHGWRNWDVYKVIYK 122
DB 83 SGMYRCQTALSTISDPVQLEVHGMWLLLTQTKWLFQEGDPIHLRCHSMQNRPRVKVYLQ 142

QY 123 DGEALKYWNENISITNATVDSGTYYCTGKWQLDYSEPLNITV 169
DB 143 NGKRGKYFHENSELPKIPKATHNDSSGYFCRGLIGHNNKSSASFRISL 189

RESULT 13
Q9BS92
ID Q9BS92 PRELIMINARY; PRT; 261 AA.
AC Q9BS92;
DT 01-MAR-2001 (TrEMBLrel. 16, Created)
DT 01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Fc gamma receptor III.
GN FCGR3.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6;
RA Fossati Jimack L., Boucrot E., Izui S.;
RT "Mouse Fc gamma RIII: identification and characterization of a new
RT allele in C57BL/6 mice.";
RL Submitted (OCT-1999) to the EMBL/GenBank/DBJ databases.
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6J; TISSUE=Ovary, and Uterus;
RX MEDLINE=22354683; PubMed=12466851;
RA The FANTOM Consortium,
RA the RIKEN Genome Exploration Research Group Phase I & II Team;

```

"Analysis of the mouse transcriptome based on functional annotation of
60,770 full-length cDNAs."

RT Nature 420:563-573(2002).
RL EMBL; AF197930; AAC28520.1; -
DR EMBL; AK072227; BAC36696.1; -
DR MGB; MGI:95500; Fcgr3.
DR GO; GO:0004872; F:receptor activity; IEA.
DR InterPro; IPR003599; IG.
DR InterPro; IPR007110; IG-like.
DR Pfam; PF00047; Ig; 2.
DR SMART; SM00409; Ig; 2.
DR PROSITE; PS00835; IG_LIKE; 2.
KW Receptor.
SQ SEQUENCE 261 AA; 30098 MW; 9C8570E032F94730 CRC64;

Query Match 36.8%; Score 349; DB 11; Length 261;
Best Local Similarity 41.3%; Pred. No. 6.9e-24;
Matches 69; Conservative 30; Mismatches 66; Indels 2; Gaps 2;

QY 4 KPKVSLNPPNRRIFKGNVTLTCGNFFVSVSTKWFHN-GSLSETRSSLNIVNAKTED 62
Db 34 KAVVLEPPNRRIFKGNVTLTCGNFFVSVSTKWFHN-GSLSETRSSLNIVNAKTED 62
QY 63 SGEYKCOHQVNESEPVYLEVFSDFWLLQASAEVVMNEGQPLFRCGWRNWDVYKVIYK 122
Db 93 SGEYRCQEQRLSDVDLGVISDWLLQTPQRFVLEGETITLRCGHWENKLNRIISFFH 152
QY 123 DGEALKYWNHNISITNATVEDSGTYCTGKWQLDYSEPLNITY 169
Db 153 NEKSVRVHHYKNSFIPKXNHSRSHGSDYCKGSLGSGTQHSKPTVITV 199

RESULT 14

QYQJ5 PRELIMINARY; PRT; 372 AA.
AC QYQJ5
DT 01-OCT-2003 (TrEMBLrel. 25, Created)
DT 01-OCT-2003 (TrEMBLrel. 25, Last sequence update)
DE High affinity IgG Fc gamma receptor 1.
GN FCGAMMARI.
OS Canis familiaris (Dog).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Carnivora; Fissipedia; Canidae; Canis.
OX NCBI_TaxID=9615;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=Shiba; TISSUE=Cutaneous;
RX MEDLINE=22777889; PubMed=12811428;
RA Nakamura R., Sato Y., Takagi K., Sasaki N., Sawada J., Kitani S.,
Teahima R.
RT "Presence and primary sequence of a high-affinity IgG receptor on
canine mastocytoma (GM-MC) cells."
RL Immunogenetics 55:271-274(2003).
DR EMBL; AB101519; BAC80263.1; -
KW Receptor.
SQ SEQUENCE 372 AA; 42336 MW; BC04026CD198049D CRC64;

Query Match 36.8%; Score 348.5; DB 6; Length 372;
Best Local Similarity 39.3%; Pred. No. 1.2e-23;
Matches 67; Conservative 33; Mismatches 67; Indels 1; Gaps 1;

QY 2 POKPVSLNPPNRRIFKGNVTLTCGNFFVSVSTKWFHNSLSEETSSLNIVNAKFE 61
Db 19 PVKAVITLQPPVSVFQESVTLWCCEGPHLPDGSQTQWFLNGATQTLTPYRIAAASVN 78
QY 62 DSGEYKCOHQVNESEPVYLEVFSDFWLLQASAEVVMNEGQPLFRCGWRNWDVYKVIY 121
Db 79 DNGEYRCQGLSVLSDFIQLGHRDWLLIQLVSGRVFTEGEPTLRCGHWENKLNRIISFFH 138
QY 122 KDGEALKYWNHNISITNATVEDSGTYCTGKWQLDYSEPLNITY 169
Db 139 QNGTVLKFPSPNSEFTILKTLHNGIYHCSA-MGKHRYESAGVSITI 185

RESULT 15

Q9N2I6 PRELIMINARY; PRT; 249 AA.
ID Q9N2I6
AC Q9N2I6
DT 01-OCT-2000 (TrEMBLrel. 15, Created)
DT 01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DB CD16.
GN CD16.
OS Felis silvestris catus (Cat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Carnivora; Fissipedia; Felidae; Felis.
OX NCBI_TaxID=9685;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=20180233; PubMed=10713347;
RA Nishimura Y., Miyazawa T., Ikeda Y., Izumiya Y., Nakamura K., Sato E.,
Mikami T., Takahashi B.;
RT "Molecular cloning and sequencing of the cDNA encoding the feline
Fc (gamma)RIIIA (CD16) homologue."
RL Vet. Immunol. Immunopathol. 73:353-359(2000).
DR EMBL; AB025314; BAA92347.1; -
DR InterPro; IPR003599; IG.
DR InterPro; IPR007110; IG-like.
DR Pfam; PF00047; Ig; 2.
DR SMART; SM00409; Ig; 2.
DR PROSITE; PS00835; IG_LIKE; 2.
SQ SEQUENCE 249 AA; 27902 MW; 683528C68A7CAB7A CRC64;

Query Match 36.7%; Score 348; DB 6; Length 249;
Best Local Similarity 42.8%; Pred. No. 8e-24;
Matches 71; Conservative 25; Mismatches 70; Indels 0; Gaps 0;

QY 4 KPKVSLNPPNRRIFKGNVTLTCGNFFVSVSTKWFHNSLSEETSSLNIVNAKTEDS 63
Db 24 KAVVLEPPNRRVLSVDGVILKCEGAYPPGDSQAQWHNGSVIPIRAPSYSEIARSEDS 83
QY 64 GEYKCOHQVNESEPVYLEVFSDFWLLQASAEVVMNEGQPLFRCGWRNWDVYKVIYKD 123
Db 84 GEYKCOQGLSEASDPVQLEVHTGWLQLQAPRVVFEGDTIQLRCHSWKNTVKQVQYFQD 143
QY 124 GEALKYWNHNISITNATVEDSGTYCTGKWQLDYSEPLNITY 169
Db 144 GRGKMFHKNDFYIPKATSKHSGSYFCRGLIGNKNSSEAVNITY 189

Search completed: October 6, 2004, 09:07:04
Job time : 28.0629 secs